

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number 11978

TO: Michael Borin

Location: rem 2a55

Art Unit: 1631

Thursday, April 22, 2004

Case Serial Number: 10/078090

From: Toby Port

Location: Biotech-Chem Library

Remsen 1A59

Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Borin,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port



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April 21, 2004, 21:08:41; Search time 703.997 Seconds (without alignments) 10740.063 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NB* PUB.seq:*

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9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

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12: /cgn2_6/ptodata/1/pubpna/US09_NB* PUB.seq:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	48, 47, 536, 782, 3728	174 406 285 285	285026 285028 285027 285027 19, Ap
Description	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence Sequence Sequence
SUMMARIES	US-10-078-090-48 US-10-078-090-47 US-10-112-944-536 US-10-094-749-782 US-10-029-386-3728	US-10-029-386-17428 US-10-120-988-406 US-10-027-632-285026 US-10-027-632-285028	US-10-027-632-285026 US-10-027-632-285028 US-10-027-632-285027 US-10-027-632-285027 US-10-087-192-19
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US-10-195-144-87	US-10-345-072-87	US-10-087-192-262	US-10-087-192-1864	US-09-997-722-67	US-10-175-523-87	US-09-799-462A-17	US-09-836-911A-17	US-09-738-630-73	US-10-125-767-17	US-10-151-081-17	US-10-287-313-17	US-10-219-694-17	US-09-910-943-3	US-10-027-632-90339	US-10-027-632-317388	US-10-027-632-90339	US-10-027-632-317388	US-10-087-192-1849	US-10-085-117-325	US-10-087-192-1831	US-10-087-192-1435	US-10-085-117-283	US-10-229-834A-6	US-09-771-208-20	US-09-997-722-85	US-09-864-761-2623	US-09-864-761-9839	US-10-087-192-1495	US-10-052-482-85	US-10-087-192-271
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75.6	75.6	74.6	74.4	73.4	73.4	73.2	73.2	73.2	73.2	73.2	73.2	73.2	73	72.8	72.8	72.8	72.8						72.2			71.8			-	71.6
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ALIGNMENTS

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1 GAGTTGCGGCGTGCCAAGGCCCACGAGGCTTGGGCTTCAGCATCCGTGGGGGCTCGGAG 60
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100.0%; Score 1677; 1
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1677; Conservative 0; Mismatches
                                                                                                                                                                                                             ORGANISM: Homo sapien
                                                                                                                                                                                   SEQ ID NO 48
LENGTH: 1677
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Oy 1201 CTGCATAGTTGCCAACAGTGTAATGTGTC Db 1201 CTGCATAGTTGCCAACAGTGTAATGTGTC Oy 1261 GGTGGCCACCTGGCCAATACACTGCACA Db 1261 GGTGGCCACCTGGCCAATACACTGCACA Db 1261 GGTGGCCACCTGGCCAATACACTGCACA Oy 1321 TCTGTGTGTGTGTGTGTGTGTGTGTGTGT	Db 1381 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1441 1501 1501 1501		RESULT 2 US-10-078-090-47 ; Sequence 47, Application US/10078090 ; Publication No. US20030044815A1	; GENERAL INFORMATION: ; APPLICANT: Salceda, Susana ; APPLICANT: Macina, Roberto ; APPLICANT: Hu, Ping) APPLICANT: Recipon, Herve) APPLICANT: Karra, Kalpana) APPLICANT: Cafferkey, Robert) APPLICANT: Sun, Yongming	, APPLICANT: Liu, Chenghua ; TITLE OF INVENTION: Compositions and Me ; FILE REFERENCE: DEX-0312 ; CURRENT APPLICATION NUMBER: US/10/078,0	CURRENT FILING DATE: 2002-02-14 ; PRIOR APPLICATION NUMBER: 60/268,999 ; PRIOR FILING DATE: 2001-02-15 ; NUMBER OF SEQ ID NOS: 210	; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 47 ; LENGTH: 667 ; TYPE: DNA	ORGANISM: Homo sapien S-10-078-090-47	Best Local Similarity 99.5%; Fred. No Misma Matches 649; Conservative 0; Misma Qy 1026 GGGGACCATAACCTGCCTCATCGCAC	16	
	241 GGGGCATCCCTGGGGGCTACGTCACCACCACTTTACACCTGGTGGACCGCAGGGC 300 241 GGGCGATCCCTGGGGGGTTCACCACCACCACTTCACACTGGGTGGACGGCGAGGGC 300 241 GGGCGATCCCTGGGGGGTTCACCACACACACTTCACACGGTGGTGGACGGCGGGGGGGG	361 GAGGGTGACCGGAGGACCACCTCCTGCAAGGAGGGATGAGAAAAAGGTGAAC 420	481 CTTGGCATTTACATCACTGGCGTGGACCCAGGCTCTGAAGCAGAAGGCAGGGGGCTCAAG 540 481 CTTGGCATTTACATCACTGGACGTGGACCCAGGCTGAAGGCAGAGGCAGCGGGCTCAAG 540 541 GTTGGCATTTACATCACTGGACGTGGACGTTTCTCAACATCTACACGACGA 600 541 GTTGGGACCAGATTCTACAAGTGATGAGCGGAAGCTTTCTCAACATCCTACACGACGA 600 541 GTTGGGGACCAGATTCTACAAGAGCGGAAGCTTTCTCAACATCCTACACGACGA 600				781 GGGCCATTICTGAAAGCCAGTGATAGCTGCCTCCCATCCCTCCACCGCCCTGGCTCTCCT 840 	841 CTCAGCCTGCAGTCCCCACACGGGCCCTCCATTGGCAGGACATGACCTGGGCACATCC 900	901 CTCTCCTCTTTGGCCTCAGTTTCCCCTGGAAAGCTGAAATACACCATCCAACTGTCTC 960 	961 ATTCHTATTGTCCCCAAATTACTTAACTCATTCTATAGACCTTAGTTGCTTCATCCAA 1020 	1021 AAAGTGGGGACCATACCCTGCCCTCATCCCGATCTGTGCAGATGAAAGAGGGGGGGG	1081 AGAGGGAAAGAGAGAGATGCTTTGGGGTGTATTTGGCCAGAGGCCACCAGGCTGGATCCC 1140 	1141 ATGAAGAAATCTGGGTGAGAGGTCTTAAAGTCATAAACTGAGATCCAGTTGCCAGGTGG 1200
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Methods Relating to Breast Specific Genes and Pr TITTGGCCAGAGGCCACGGCTGGATCCCATGAA 1145 . 0 AGATCTGTGCAGATGAAAGAGGGAGGGAGGAGG 1085 TATRARARARARCAGCTGCCTCTCTGCATAG 1500 GGACAGCGGACAAAACCACGTGAGGGAGCAACA 1620 GRENGRETGREGREGERGEGECCCCCA 1380 CACCTITIGATCITCATCAGAAATCICAGGCT 1260 1320 BAGCATGTCTGTCTGTCTGTCTGTGTCTC 1320 ACACGTGAAAAAGCGAGACCAGGGGGGGAGA 1677 647.2; DB 15; Length 667; No. 2e-177; matches 3; Indels 0; Gaps Agcargrererererererererererer

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                                                                                                                                                                                                                                                                                                                                                                                                     DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                 33.1%; Score 554.8; DB 13
99.6%; Pred. No. 3.9e-150;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 782, Application US/10094749;
Publication No. US20030219741A1
GENERAL INFORMATION: TAKAO
APPLICANT: SIGGAI, TAKAO
APPLICANT: SUGITYAMA, TOMOYASU
APPLICANT: WAKAMATSU, AI
APPLICANT: WAKAMATSU, AI
APPLICANT: STO, HIROYUKI
APPLICANT: SANO, HIROYUKI
APPLICANT: SANO, WUNKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: IREA KAORU
APPLICANT: TAMAMOTO, TUNICA
APPLICANT: TAMEA, KRIICHI
APPLICANT: TAMEA, KAORU
APPLICANT: TAMECHIKA, ICHIRO
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
SEG ID NO 536
LENGTH: 2964
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Best Local Similarity 99.6
Matches 556; Conservative
                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Homo sapiens
US-10-112-944-536
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                1146 GAAATCTGGGTGAGGGTCTTAAAGTCATAAACTGAGATCCAGTTGCCAGGTGGCTGCA 1205
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                                                                                                                                                                                                                         196 TAGTIGCCAACAGIGTAATGIGTCACCTTTTGAICTTCAICAGAAATCTCAGCGGGGG
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                                                                   1626 GGGGGGAACCACATTACCCCACACACGTGAAAAAGCGAGACCAGGGGGGAGA 1677
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APPLICANT: Tang, Y. Tom

APPLICANT: Yang, Y. Orghong

APPLICANT: Weng, Gezhi

APPLICANT: Ren, Reiyan

APPLICANT: Ren, Reiyan

APPLICANT: Ren, Reiyan

APPLICANT: Weng, Jian-Rui

APPLICANT: Wang, Dunrui

APPLICANT: Wang, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 536, Application US/10112944 Publication No. US20040048249A1 GENERAL INFORMATION:
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US-10-029-386-17428

US-10-029-386-17428

Sequence 17428, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Fent, Sharron G.

APPLICANT: Hanzel, David R.

APPLICANT: APPLICANTON: WINDER: US/10/029,386

CURRENT APPLICATION UNDER: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 17428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 GETCACCAACCACATCTACACCTGGGTGGACCCGCAGGGCCGCAGCATCTCCCCACCTC
                                                                                                                                                                                                                                                                                                                                                                                             81 GICTCTGGTGGAACCAGGCTCTCTAGCTGAGAAGGAAGGACTGCGGGGACCAGAT
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL138895.4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.63
OTHER INFORMATION: EST HUMAN HIT: BE890168.1, EVALUE 1.00e-105
OTHER INFORMATION: MIT HIT: 9114735271, EVALUE 1.00e-106
OTHER INFORMATION: SWISSPROT HIT: P35428, EVALUE 3.70e-01
US-10-029-386-17428
                                                                                                                                                                                                                                                                                            Query Match 14.4%; Score 240.8; DB 15; Length 509; Best Local Similarity 77.1%; Pred. No. 3.2e-59; Matches 293; Conservative 0; Mismatches 87; Indels 0;
                                            TYPE: DNA

PEATURE:

CHER INFORMATION: MAP TO AL138895.4

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.63

OTHER INFORMATION: THIT: 9114735271, EVALUE 1.006-123

OTHER INFORMATION: EST HUMAN HIT: BF969269.1, EVALUE 0.006+00

OTHER INFORMATION: SWISSPROT HIT: P54817, EVALUE 3.706-02

US-10-029-386-3728
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  SEQ ID NO 3728
LENGTH: 509
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US-10-029-386-3728
US-10-029-386-3728
Sequence 3728, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David K.
APPLICANT: RANK, David K.
APPLICANT: HARZEL, DAVIG K.
APPLICANT: HARZEL, DAVIG K.
APPLICANT: ADDITOR: SERESION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1436 GGTGACCGGAGGAGCACCCTGCACCTCCTGCAAGGGGGGATGAGAAAAAGGTGAGTGGG 1495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 420.2; DB 16;
Pred. No. 4.1e-111;
0; Mismatches 23;
APPLICANT: SEKI, NACHIKO
APPLICANT: OYGHIKANA, TSUTOMU
APPLICANT: OYSHIKAN, TSUTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: NACAHARI, KENJI
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REPERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-03-14
FRIOR FILING DATE: 2002-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATCHING DATE: 2010-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATCHING DATE: 2010-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATCHING DATE: 2010-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 95.0%;
Matches 434; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-782
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969 rerdaktractrecideciredacedacereadedacedededecreeadeaderefecedeec 1028 849 AACGGTGTCAGGTTTGACGACATCAGCCACAGCCCGTGGAGGGTGCTGAAGGGCCCAA 908 909 acecacarcarecreacearcaacaaccescoscarrecracaacaacaacarecri 968 685 GACGAGACCAAGTGGGTCGCCAGTTCCCGGATCAGGGAGACCATGGCGAACTCGGCAGGG 744 648 GGTTCAACACCCTCC----GACACCAGCTCAGÁAGÁTGGTGTCCGGCGATGGTCCAC 701 GENERAL INVENTION:
GENERAL INVENTION:
GENERAL INVENTION:
GENERAL INVENTION:
JULIANT:
MANAGO, DAVIG G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: DOLYMORPHISMS in the Human Genome
FILE REFERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/02/04-30
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1099-108-67
PRIOR PILING DATE: 1099-09-28
PRIOR PILING DATE: 1099-09-28
PRIOR PILING DATE: 1999-09-38
PRIOR PILING DATE: 1999-09-38
PRIOR FILING DATE: 1990-09-38
PRIOR FILING DATE: 1990 789 gaccanderedecedadadadandecarcaaderededacacadededecedece CTGCCCCAGCCCCACGGTGCCCTGAGGCAGCAGGAGGGTGACCGGAGGAGCACCCTG -----ACAACCTCCGACGACTTCTGC 445 CTGGGCCTCACGATCCGTGGGGGAGCTGAGTACGGCCTTGGCATTTACATCACTGGCGTG GACCCAGGCTCTGAAGCAGAAGGCAGCGGGCTCAAGGTTGGGGACCAGATTCTAGAAGTG 565 AATGGGCGGAGCTTTCTCAACATCCTACACGAGGCTGTCAGGCTGCTTAAGTCATCT 625 COGCACCTCATCCTGACAGTGAAGGACGTCGGGAGGCTGCCCCATGCCCGCACCACTGTG CACCTCCTGCAAGGAGGGGATGAGAAAAAGGTGAACCTGGTGCTGGGGGACGGCCGGTCC Length 553; Indels Query Match
4.6%; Score 76.6; DB 13;
Best Local Similarity 64.2%; Pred. No. 2.1e-11;
Matches 115; Conservative 0; Mismatches 64; Sequence 285026, Application US/10027632 publication No. US20020198371A1 GENERAL INFORMATION: CTATAC-----, ORGANISM: Human US-10-027-632-285026 RESULT 8 US-10-027-632-285026 343 505 385 702 à d 임 8 8 8 ò g 8 8 8 음 8 8 q 85 CTGGTGGAACCAGGCTCTCTAGCTGAAGGAAGGACTGCGGGTCGGGAACCAGATTCTG 144 408 papatredanganaedengeneriekadadengeerredeerreregregegeneradantened 467 CGCGTCAACGACAAATCCCTGGCCCGGGTGACCCACGCGGAGGCCGTCAAGGCTCTGAAG 204 468 GAGGIGAATGGGCTGAGCCTGGAGAGCACCACCATGGGTAGCGCCGTAAAGGTGCTGACC 527 205 GGCTCCAAGAAGCTGGTGTGTGTGTACTCAGGAGGCGCATCCCTGGGGGGTACGTC 264 528 adcadchaccacchacacahdanadhncacacanadaccdnahachdancaadhid 587 265 ACCAACCACATCTACACCTGGGTGGACCCGCAGGGCCGCAGCATCTCCCCACCCTCGGGC 324 ö 61 GGCTACGTCACCAACCACATCTACACCTGGGTGGACCCGCAGGGCCGCAGCATCTCCCCAA 120 CCCTCGGGCCTGCCCCAACGCTGGTGCCCTGAGGCAGCAGGAGGGTGACCGGAGG 375 25 GAGGGCTTGGGGCTTCAGCATCCGTGGGGGCTCGGAGCACGGCGTGGGCATCTACGTGTCT Query Match 6.4%; Score 107.6; DB 16; Length 2822; Best Local Similarity 49.9%; Pred. No. 5.3e-20; Matches 361; Conservative 0; Mismatches 324; Indels 39; Gaps 196 GCTCTGAAGGGCTCCAAGAAGCTGGTGTGTGTTGTTGTCTCAGCAGGCGCATCCCTGGG <u>ecrerandadecrecandanaeriearecrarerarararerendadedededecarecerade</u> GGCTACGTCACCAACCACATCTACACCTGGGTGGACCCGCAGGGCCGCAGCATCTCCCCA Gaps ö APPLICANT: TOOM
APPLICANT: Goodrich, Ryle
APPLICANT: Goodrich, Ryle
APPLICANT: Goodrich, Ryle
APPLICANT: Loc Chenghua
APPLICANT: Nen, Felyan
APPLICANT: Nen, Felyan
APPLICANT: Neng, Dunrul
APPLICANT: Neng, Dunrul
APPLICANT: Dramanc, Radoje T.
ITLE OF INVENTION: No. UGS0030219745A1e1 Nucleic Acids and
ITLE OF INVENTION: No. UGS0030219745A1e1 Nucleic Acids and
ITLE REFERENCE: 802CON
UNRENT PAPLICATION NUMBER: US/10/120,988
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 09/774,528
FROR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: PL_Genes Version 2.0 Indels 100.0%; Pred. No. 3.8e-46; tive 0; Mismatches 0; Sequence 406, Application US/10120988; Publication No. US20030219745A1; GENERAL INFORMATION: 376 AGCACCCTGCACCTC 390 Conservative TYPE: DNA ORGANISM: Homo sapiens ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (66)..(2822) US-10-120-988-406 Best Local Similarity Matches 195; Conserv 145 256 316 g 8 G 8 8 ò g ઠે 셤 8 8 ઠે g ò ò

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Sequence 285028, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
JTTLE OF INVENTION:
JTTLE OF INVENTION:
FILE REPERENCE: 108827.129

CURRENT PILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/18,006

PRIOR APPLICATION NUMBER: US 60/18,006

PRIOR APPLICATION NUMBER: US 60/18,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,383

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/165,363

PRIOR APPLICATION NUMBER: US 60/166,358

PRIOR APPLICATION NUMBER: US 60/166,358

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002
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US-10-027-632-285026

US-10-027-632

Sequence 285026, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REPRENCE: 10827-129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US/200-04-30

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12
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Pred. No. 2.1e-11;
0; Mismatches 64;
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Best Local Similarity 64.2%;
Matches 115; Conservative
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US-10-027-632-285028
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PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28

; TYPE: DNA ; ORGANISM: Human US-10-027-632-285026

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US-10-27-632-286028

Sequence 285028, Application US/10027632

Sequence 285028, Application No. US20030204075A9

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT PILICA DATE:
CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US/00.04

PRIOR PILING DATE: 2002-04-30

PRIOR PILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 1999-10-23

PRIOR FILING DATE: 1999-10-23

PRIOR FILING DATE: 1999-10-38

PRIOR FILING DATE: 1999-10-38

PRIOR FILING DATE: 1999-10-38

PRIOR FILING DATE: 1999-10-38

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PRIOR FILING DATE: 1999-10-38

PRIOR FILING DATE: 1999-10-38

PRIOR FILING DATE: 1999-10-38

PRIOR FILING DATE: 1999-10-38

PRIOR FILING DATE: 1999-09-28

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5; DB 16; Length 553;
2.1e-11;
                                                                                              Indels
                          Score 76.6; Di
Pred. No. 2.1e
0; Mismatches
                              4.6%;
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Best Local Similarity 64.2
Matches 115, Conservative
                              Query Match
Best Local Similarity 64.2
Matches 115; Conservative
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; ORGANISM: Human
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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-285027
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Fublication No. US2020198371A1

Fublication No. US2020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT APPLICATION: UNBER: US 60/218,006

FRIOR FILING DATE: 2000-07-12

FRIOR FILING DATE: 2000-07-12

FRIOR FILING DATE: 2000-04-20

FRIOR PRICATION NUMBER: US 60/183,483

FRIOR FILING DATE: 2000-03-29

FRIOR PRILOR APPLICATION NUMBER: US 60/185,218

FRIOR FILING DATE: 1099-11-23

FRIOR FILING DATE: 1099-11-23

FRIOR FILING DATE: 1099-11-23

FRIOR FILING DATE: 1099-109-28

FRIOR FILING DATE: 1099-09-28

FRIOR FILING DATE: 1999-09-28

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Publication No. US20030204075A9;
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide;
TITLE OF INVENTION: Polymorphisms in the Human Genome;
FILE REFERENCE: 108827.129
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1299 ICTGICTGICTGICTGIGICTCICTGIG
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Matches 114; Conservative
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US-10-027-632-285027
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CRGANISM: Human
US-10-027-632-285027
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1419 ATATTAGAGAGATACACAGAAATATATAGAGAAGATAACAGTGTTCTCTATAAAAA 1477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.5%; Score 76.2; DB 16; Length 63.7%; Pred. No. 2.7e-11; ive 1; Mismatches 64; Indels
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US-10-08-192-19
Squence 19, Application US/10087192
Squence 19, Application US/10087192
Squence 19, Application US/10087192
Squence 19, Application No. US2002018286A1
APPLICANT: Bright NovEL CANDOSTITIONS AND METHODS FOR ITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR ITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR ITLE OF INVENTION: NOVER: 2002-03-01
PRIOR PELLING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastESQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 113633
TYPE: DNA
PRIOR MUS musculus
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4.5%, Score 76.2; DB 13;
Best Local Similarity 96.3%; Pred. No. 6.9e-10;
Matches 78; Conservative 0; Mismatches 3;
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PLING DATE: 2002-04-30
PRIOR PLING DATE: 2000-07-12
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PRING DATE: 2000-03-29
PRIOR PLING DATE: 1990-03-24
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PRING DATE: 1999-09-28
PRIOR PRING DATE: 1999-09-09
PRIOR PRING DATE: 1999-09-09
PRIOR PRING DATE: 1999-09-09
SOFTWARR: FRAEKEQ FOR WINGOWS VERSION 4.0
SSOFTWARR: FRAEKEQ FOR WINGOWS VERSION 4.0
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NAME/KEY: misc_feature
LOCATION: (1)...(113633)
CTHER INFORMATION: n = A,T,C or G
US-10-087-192-19
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Matches 114; Conservative
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us-10-078-090-48.rnpb
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RESULT 15
US-10-195-144-87/C
i Sequence 87, Application US/10195144
j Fublication No. US20030126646A1
j Fublication No. US20030126646A1
j GENRRAL INFORMATION;
j APPLICANT: BROWN, GREGORY G.
j APPLICANT: BROWN, CHARLES
j APPLICANT: LANDRY, BENOIT S.
j APPLICANT: LANDRY, BENOIT S.
j APPLICANT: LANDRY, BENOIT S.
j APPLICANT: LANDRY, BENOIT S.
j APPLICANT: UNWENT: US/10/195,144
j TILLE OF INVENTION: PLANTS
j FILLE REFERENCE: 16313-0136
j CURRENT PILING DATE: 2002-10-01
j PRIOR PILING DATE: 2001-07-12
j PRIOR APPLICATION NUMBER: 60/305,026
j PRIOR APPLICATION NUMBER: 60/305,363
j PRIOR APPLICATION NUMBER: 60/305,363
j PRIOR PILING DATE: 2001-07-13
j PRIOR APPLICATION NUMBER: 60/305,363
j PRIOR FILING DATE: 2001-07-13
j PRIOR PILING DATE: 2001-07-30
j NUMBER OF SEQ ID NOS: 128
j SEQ ID NO 87
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TGTGTGTGTGTGTGTGTGTGTGTG 1352
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4.5%; Score 75.6; DB 15; Length 271990;
Best Local Similarity 65.3%; Pred. No. 1.7e-09;
Matches 111; Conservative 0; Mismatches 59; Indels 0;
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LOCATION: (144241)..(144300)
OTHER INFORMATION: a, t, c, g, other or unknown
US-10-195-144-87
Search completed: April 22, 2004, 01:59:54 Job time : 707.997 secs
                                                                                                     45422 TGTGTGTGTGTGTGTGT 45442
                                                                                 1353 TGTGTGTGTGTGTGTGT 1373
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ORGANISM: Raphanus sativum
FEATURE:
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OM nucleic - nucleic search, using sw model	April 21, 2004, 19:28:36; Search time 2576.09 Seconds (without alignments) 11222.365 Million cell updates/sec	US-10-078-090-47 score: 667 e: 1 gcgtggtcgcggcccgaggtaagcgagaccaggggggaga 667	table: IDENTITY_NUC Gapop 10.0, Gapext 1.0	d: 3470272 seqs, 21671516995 residues	Total number of hits satisfying chosen parameters: 6940544	Minimum DB seq length: 0 Maximum DB seq length: 200000000
OM nucleic - m	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Total number o	Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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gb bag: *
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Pred. No. is the number of results predicted by chance to have a

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SUMMARIES

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AL138895/c LOCUS DEFINITION

ALIGNMENTS

AL138895
Human DNA sequence from clone RP11-9M16 on chromosome 9, complete sequence.
AL138895
AL138895.16 GI:14575083
HTG.
Homo sapiens (human)
Homo sapiens (human)
Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 132292)
Skuce, C.
Direct Submission

REFERENCE AUTHORS TITLE

COMMENT

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repeat_region
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                                                                               inquences: clouetrequesteranger.ac.ux
On Jun 28, 2001 this sequence version replaced gi:14456172.
During sequence assembly data is compared from overlapping clones.
During sequences are found these are annocated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Emb.; Sw.; SWISSPROT; Tr.; TRENBL; WORMPEP; Information on the WORMPEP there are not a second to associate primary accession numbers of the accession of the wormpressions of the second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a second to a 
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Submitted (27-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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7271. 2435

700te="WER63A repeat: matches 46. 206 of consensus"

70te="WIR repeat: matches 79. 165 of consensus"

7887. 2313

70te="L2 repeat: matches 2622. 2740 of consensus"
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note="Alusc repeat: matches 5. .301 of consensus"
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note="MIR repeat: matches 115. .166 of consensus"
1193. .4262
note="MIR repeat: matches 60. .130 of consensus"
368. .5308
note="CpG island"
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note="AluSq repeat: matches 1. 298 of consensus"
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note="MIR repeat: matches 49. .142 of consensus"
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/note="MIR repeat: matches 141.
6714. .6799
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="9"
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/clone_lib="RPCI-11.1"
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18972. Layusu
Taote="MIR repeat: matches 34. .144 of consensus"
18542. .20994
Thote="Charlie4a repeat: matches 26. .506 of consensus"
18121. .21521
                                                                                                                                                              1160, .8271
|note="LTR16C repeat: matches 255. .368 of consensus"
| 0037, .10131
                                                                                                                                     .354 of consensus'
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15702 1595
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16704="12 repeat: matches 2372. .2688 of consensus"
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1685. 16842
1685. 16922
16875. 16922
17875. 16922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2289 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2709 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="u2 repeat: matches 2363. .2674 of consensus"
16257. .26381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21421. 21521

10cte="12 repeat: matches 2045. .2158 of consensus"

21523. -21758

7note="AluJo repeat: matches 1. .232 of consensus"

2863. -23243

7note="WRTA repeat: matches 1. .426 of consensus"

23119. .23495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102. .254 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .298 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MERSB repeat: matches 1. .173 of consensus"
                                                                                                                                                                                                                        note="MIR repeat: matches 14. .123 of consensus"
.0604. .10711
note="L2 repeat: matches 2405. .2521 of consensus"
.1151. .11327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="LZ repeat: matches 2593. .2734 of consensus 29669. .29777
7note="MIR repeat: matches 17. .140 of consensus"
                                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 18. .205 of consensus"
11579. .11883
/note="AluSx repeat: matches 1. .304 of consensus"
11886. .12024
/note="MIR repeat: matches 97. .243 of consensus"
12598. .12717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note="MIR repeat: matches 5. 192 of consensus" 4438. 24542
14438. 24542
Note="MIR repeat: matches 28. 140 of consensus" 25526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .230 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MIR repeat: matches 16. .262 of consensus" 5889 ____26233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="MIR repeat: matches 28. .153 of consensus"
.6919. .27000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       consensus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8153. 120377
notes "MIR repeat: matches 23. 241 of consensus"
8972. 19080
                         8995. ,7437
/note="MLT1D repeat: matches 3. .503 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="MIR repeat: matches 80. .258 of consensus" 4011. .14205
                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MIR repeat: matches 52. .181 of consensus"
1839, .14002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .226 of consensus"
                                        7440. .7502 ....matches 82. .144 of consensus 8034. .8179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anote="MIR repeat: matches 64. .147 of 27292. 27435
//note="MIR repeat: matches 102. .254 of 29060. .29388
벙
                                                                                                                 1034. .8179
note="LTR16A repeat: matches 200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L2 repeat: matches 2099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L2 repeat: matches 2167.
30460. .30627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MIR repeat: matches 125.
8163. .18379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |4071. .14205
|note="MIR repeat: matches 92.
|5216. .15653
repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .30243
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us-10-078-090-47.rge

20 H 0 D H 50 Z	TITLE Direct Submission JOURNAL Submission JOURNAL Submission Submission Submission NOTE: This is a "working draft" sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. * 804 903: contig of 803 bp in length * 804 8454: contig of 7551 bp in length * 8455 8554: gap of unknown length * 8455 171627: contig of 163073 bp in length * 8555 171627: contig of 163073 bp in length * 8555 171627: contig of 163073 bp in length * 8555 171627: contig of 163073 bp in length * 8555 171627: contig of 163073 bp in length * Anolypa="gap of unknown length" * Anolypa="gap of unknown length" * RATURES * 1171627: contig of 163073 bp in length * Anolypa="gap of unknown length"		OY 16 GAGGTCCATAACCCTGCCCTCATCCCAGATCTGTGCAGATGAAAGAGGGAGGGA 71	Oy 132 TGAAGAAATCHGGGTGAGAGGGTCTTAAAGTCATAAACTGAGATGCAGGTGGC 191	Oy 252 GIGGCCACCTGGCCAATACACTGCAGAGCATGTCGTCTGTCT
repeat_region 3065830770 Inote="L2 repeat: matches 25722690 of consensus" Inote="L2 repeat: matches 25142731 of consensus" Inote="L2 repeat: matches 25142731 of consensus" 3209532170 Inote="15 copies 4 mer acac 88% conserved" Inote="16 copies 2 mer tc 84% conserved" 3242632485 Inote="Min repeat: matches 96152 of consensus" Inote="Min repeat: matches 96152 of consensus" Inote="Min repeat: matches 4281 of consensus" 3349433764 Inote="Aludo repeat: matches 26412709 of consensus" Inote="Aludo repeat: matches 1293 of consensus" Inote="Aludo repeat: matches 1293 of consensus" Inote="Aludo repeat: matches 1293 of consensus" Inote="Aludo repeat: matches 1293 of consensus" Inote="Aludo repeat: matches 1293 of consensus" Inote="Min repeat: matches 8207 of consensus" Inote="Min repeat: matches 8207 of consensus" Inote="Min repeat: matches 8207 of consensus" Inote="Min repeat: matches 8207 of consensus"	peat: matches 1303 cat: matches 2147 of peat: matches 1188 cat: matches 49140 of at: matches 14252 of at: matches 26712750 cat: matches 98126 of at: matches 46126 of at: matches 46126 of at: matches 46146 of act: mat	0; Mismatches CTCATCCCAGATCTGTGC 	Oy 76 GAAAGAGAGATGCTTTGGGGTGTATTTGGCCAGAGGCCACCAGGTCGATCCCATGA 135	QY 196 TAGTTGCCAACAGTGTAATGTCACCTTTTGATCTTCATCAGAAATCTCAGCCTGGTGG 255 Db 32256 TAGTTGCCAACAGTGTAATGTGTCACCTTTTGATCTTCATCAGAAATCTCAGGCTGG 32197 QY 256 CCACCTGGCCAAATACACTGCAGAGCATGTCTGTCTGTCT	Qy 316 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Orpriniformes; Cypriniformes; Danio.

1 (bases 1 to 2093)

2 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Rlausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buttow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K.F., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, F.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, Y.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M., Sanchez, M., Wallek, J.A., Gunaratne, P.H., Richards, S., Sanchez, A., Whiting, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Rodrigues, S., Shoutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Schmutz, J., Myers, R.M., Schein, J.E., Young, A., Schein, J.E., J., Schmutz, J., Myers, R.M., Schein, J.E., Young, A., Schein, J.E., J., Schmutz, J., Myers, R.M., R., Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002) 100840 CTTCCCTTCCTTTC-----ACCTGCATAGTATTAAACATTTTCAAAGTTACTTGCCAA 100788 2093 bp mRNA linear VRT 07-OCT-2003 Danio rerio cDNA clone MGC:56117 IMAGE:5411459, complete cds. BC051776 BC051776.1 GI:30353803 MGC. 372 TCTTTCATCCTATCATTACATAGTAGTATAATAATAATAATTAGAGAGATACACAGAAAA 431 Classes 1 to 2093)
Strausberg,R.
Birect Submission
Submitted (01-MAY-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, 100787 CATCTAGAAGATACCAGGTTTTCTATAAAAAAAAA 100750 432 TATATAGAGAAGATAACAGTGTTCTCTATAAAAAAAA 469 Danio rerio (zebrafish) Danio rerio 12477932 RESULT 3
BC051776
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS JOURNAL REMARK TITLE COMMENT à 유 ઠે 셤

Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 103 Row: f Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

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ATLRSAPQDP" 1937 IGIGIGIGIGIGIGIGIGIGIGIGIGITITGIGITIATAACTGCATTAAAATACACTCT 1996 0 333 IGTGIGTGIGTGIGTGIGTGIGTGIGTGIGTGIGTCTCCTCACTCTTTCATCCTATCATTACAT 392 393 AGTAGTATAATAATATATTAGAGAGATACACAGAAAATATATAGAGAAGATAAACAGTG 452 Gaps 0; Length 2093; Query Match
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Matches 131; Conservative 0; Mismatches 69; Indels /organism="Danio rerio"

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RESULT 4 AC135372

Rattus norvegicus clone CH230-329KlO, *** SEQUENCING IN PROGRESS AC135372 AC135372.1 GI:23928474 HTG; HTGS_PHASE1. Kattus norvegicus (Norway rat) Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION REFERENCE ACCESSION

FEATURES

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6421: gap of unknown length 7606: contig of 1605 bp in length 9297; gap of unknown length 11743: contig of 1591 bp in length 11743: contig of 1406 bp in length 11871: contig of 1406 bp in length 11871: contig of 1000 bp in length 11871: contig of 1000 bp in length 11871: gap of unknown length 11871: gap of unknown length 11874: contig of 1219 bp in length 11874: contig of 1219 bp in length 11874: contig of 1219 bp in length 11874: contig of 1219 bp in length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unknown length 11875: gap of unk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft' sequence. It currently consists of 66 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1002: contig of 1002 bp in length
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2267: contig of 1165 bp in length
2367: gap of unknown length
3779: contig of 1412 bp in length
5869: contig of 1189 bp in length
5168: gap of unknown length
5168: gap of unknown length
6321: contig of 1153 bp in length
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11103
22268
2368
3780
5069
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JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
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COMMENT

Park

4444 Forest

Park

4444 Forest

63108, USA

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Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (21-UUN-2002) Genome Sequencing Center, 4444 Forest Park
Barkway, St. Louis, MO 63108, USA
6 (bases 1 to 214625)
Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J meuose kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEICHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone. This clone
overlapped by AC111085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (05-NOV-2003) Department of Genetics, Washington Submitted (05-NOV-2003) Department, St. Louis, Missouri 63 On Jun 21, 2002 this sequence version replaced gi:20389758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Washington University Genome Sequencing Center
Center code: WUGSC
McPherson, J. D. and Waterston, R. H.

Direct Submission
Submitted (129-MSR-2002) Genome Sequencing Center, 444-
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 214625)
McPherson, J. D. and Waterston, R. H.
Direct Submission
Submitted (02-MSY-2002) Genome Sequencing Center, 444-
Parkway, St. Louis, MO 63108, USA
Farkway, St. Louis, MO 63108, USA
S. (bases 1 to 214625)
McPherson, J. D. and Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: M_BA0340C13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. 214625
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                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
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Mus musculus BAC clone RP23-340C13 from 9, complete sequence.
AC116582
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 214625)
VanBrunt, A., Bielick; L. and Doebber, A.
The sequence of Mus musculus BAC clone RP23-340C13
Unpublished (2001)
2 (bases 1 to 214625)
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Matches 192; Conservative
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Anote="Sequence derived from one plasmid subclone." 3411. .3419 /note="Sequence derived from one plasmid subclone."

unsure unsure

Sequencing of Mus musculus Unpublished (2001)

Wilson, R

AUTHORS TITLE JOURNAL

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REFERENCE AUTHORS TITLE JOURNAL

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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Danio rerio clone CH211-218021, WORKING DRAFT SEQUENCE, 5 unordered
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Danio rerio (zebrafish)
Danio rerio (zebrafish)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Cypriniformes; Cyprinidae; Danio.
Cypriniformes; Cyprinidae; Danio.
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Matches 137; Conservative 0; Mismatches 82; Indels 0;
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               Direct Submission

Submitted (03-4002-2003) Wellcome Trust Sanger Institute, Hinxton,
Submitted (03-4002-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 15A, UK. E-mail enquiries:
Zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 4, 2003 this sequence version replaced gi:31746336.
                                                                                                                                                    Center: Wellcome Trust Sanger Institute
Center code: SC Trust Sanger Institute
Center code: SC Trust Sanger ac.uk
Website: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
Conter project Information
Center project Information
Center project Institute
Assembly program: XGAP4, version 4.5
Chemistry: Dye-terminator: 100% of reads
Consensus quality: 209702 bases at least Q40
Consensus quality: 209702 bases at least Q20
Consensus quality: 200705 bases at least Q20
Insert size: 211188; sum-of-contigs
Insert size: 208675; S.8% error; agarose-fp
Quality coverage: 8.52x in Q20 bases; sum-of-contigs
Quality coverage: 8.52x in Q20 bases; sum-of-contigs
Coverage: 8.81x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2651: contig of 2651 bp in length

652 2751: gap of 100 bp

752 121494: contig of 118743 bp in length

495 121594: gap of 100 bp

655 128045: contig of 6451 bp in length

646 128145: gap of 100 bp

146 130387: contig of 2242 bp in length

146 130387: contig of 2242 bp in length

148 211588: contig of 81101 bp in length.

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fnote=sasembly_fragment:00992
fragment_chain:1"
130488. 211588
fnote=sasembly_fragment:01224
fragment_chain:1
clone_end:17
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[ragment_chain:1"
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-218021"
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone mame. Note that the variation amoration may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROY; Tr;, TREMBL; Wp;, WORMPBP; Information on the WORMPBP database can be found at the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm
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AL732512 46643 bp DNA linear ROD 30-JUL-2002 Mouse DNA sequence from clone RP23-21G12 on chromosome 4, complete
                                                                                                                                                                                                                            Mus musculus (house mouse)
Wus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (30-701-2002) Wellcome Trust Sanger Institute, Hinxton, Submitted (30-701-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 183, UK. B.mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 31, 2002 this sequence version replaced gi:22003179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/clone lib≈"RPCI-23"
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AL732512.7 GI:22035710
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Phillimore, B.
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13.0%; Score 86.6; DB 2; Length 211588; 73.8%; Pred. No. 4.3e-12; tive 0; Mismatches 39; Indels 0;

Matches 110; Conservative

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Query Match Best Local Similarity

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L. Daese I to 166893

E. Chaese I to 166893

E. Attori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
391 ATAGTAGTATAATAATATATTAGAGAGATACACAGAAAATATATAGAGAAGATAACAG
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Homo sapiens
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453 ITCICIATAAAAAAAAAGGG 474

393 AGTAGTATAATAATAATATTAGAGAGATACACAGAAAATATATAGAGAAGATAACAGTG

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence than one subclone; and the assembly was confirmed by restriction diest.

MAPPING INFORMATION:

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Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
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The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org SOURCE INFORMATION:

NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone.
Location/Qualifiers
Location/Qualifiers
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repeat_region

Query Match 12.8%; Score 85.2; DB 10; Length 179355; Best Local Similarity 70.4%; Pred. No. 9.9e-12; Matches 114; Conservative 0; Mismatches 48; Indels 0; (

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0; Gaps

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                                                GTGTGTGTGTGTGTGTGTGTGTCTCCTCACTCTTTCATCCTATCATTACATAGTAG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (18-OCT-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 20, 2003 this sequence version replaced gi:35210297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Schinopterygii; Neopeerygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1. (bases 1 to 213715)
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Chemistry: Dye-terminator; 100% of reads
Consensus quality: 21009 bases at least Q40
Consensus quality: 210094 bases at least Q40
Consensus quality: 210994 bases at least Q20
Insert size: 212915; sum-of-contigs
Constitution of the contige part of the contige part size: 205869; 2.4% error; agarose-fp
Quality coverage: 10.08x in Q20 bases; sum-of-contigs Quality
coverage: 10.65x in Q20 bases; agarose-fp
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                                                                                                                                                                                                113110 AATACACATATGATAAAGAAATTAGAAACAGTACATAGA 113151
                                                                                                                                                     398 TATAATAATAATATTAGAGAGATACACAGAAAATATATAGA 439
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BX649528.2 GI:37776948
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Danio rerio (zebrafish)
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Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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BX649528/c
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DEFINITION
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AUTHORS
TITLE
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BX122566 203271 bp DNA linear HTG 02-JUN-2003 Danio rerio clone CH211-209B6, WORKING DRAFT SEQUENCE, 2 unordered
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                                                                                                                                                                                                                                           Gaps
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Best Local Similarity 54.9%; Pred. No. 1e-11;
Matches 168; Conservative 0; Mismatches 138; Indels
BX322566.2 GI:30724826
HTG: HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Danio rerio (zebrafish)
Danio rerio
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misc feature

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FEATURES

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                                                                                                                       Submitted (28-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: Zish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On May 14, 2003 this sequence version replaced gi:29500751.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60; Indels
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                                                                                                                                                                                                                                 Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
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Cypriniformes; Cyprinidae; Danio.
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                                                                                                         Direct Submission
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BX530074 11near HTG 29-SEP-2003 2 215778 bp DNA linear HTG 29-SEP-2003 Danio rerio clone DKEY-266K15, WORKING DRAFT SEQUENCE, 7 unordered
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Submitted (28-SEP-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CBIO 15A, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: Clonerequest@sanger.ac.uk
On Sep 29, 2003 this sequence version replaced gi:32134827.
                                                                                           BX530074
BX530074.3 GI:37051046
HTG; HTGS PAASE1; HTGS DRAFT; HTGS_FULLTOP.
Danio rerio
Danio rerio
Danio rerio
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Actinopterygii: Lospinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces * is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * trus of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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78 2157778: contig of 8901 bp in length.
Location/Qualifiers
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1. 4918
1. 00ce=sseembly_fragment:01270
fragment_chain:1"
5019. .71913
/note="assembly_fragment:02287
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/clone="DKEY-266K15"
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RESULT 12
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                         Sequencing vector: M13, 0%
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Sequencing vector: M13, 0%
Sequencing vector: M13, 0%
Sequencing vector: M13, 0%
Chemistry: Dye-terminator B1g Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 133243 bases at least Q40
Consensus quality: 133242 bases at least Q20
Insert size: 244000; agarose-fp
Insert size: 137644; sum-of-contigs
Quality coverage: 15.35 in Q20 bases; sum-of-contigs
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5857. .12184
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26085. .45068
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45169. .79414
/note="assembly_name:Contig22"
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/organism="Mus musculus"
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McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (24-JAN-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, Mo 63108, USA
3 (bases 1 to 135904)
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Submitted (24-SB2-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 631.08, USA
On Sep 24, 2003 this sequence version replaced gi:28557977.
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AC139157.3 GI:35069405
AC139157.3 GI:35069405
MUS musculus (house moüse)
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 135904)
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12.7%; Score 85; DB 2; Length 215
Best Local Similarity 66.9%; Pred. No. 1.1e-11;
Matches 121; Conservative 0; Mismatches 60; Indels
The sequence of Mus musculus clone
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                                                                               ACI30218 213673 bp DNA linear ROD 19-NOV-2003
Mus musculus chromosome 18 clone RP23-121N18, complete sequence.
ACI30218
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Direct Submission
Direct Submission
Direct (19-NOV-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On Nov 19, 2003 this sequence version replaced gi:28604207.
                                                                                                                                                                            Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Mases I to 213673)
Wilson,R.K.
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McPherson, J. D. and Waterston, R. H.

Millert Submission

Submitted (0.8-Mid-2002) Genome Sequencing Center, 4444 Forest Park

Parkway, St. Louis, MO 63108, USA

J. Chases 1 to 213673)

McPherson, J. D. and Waterston, R. H.
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Submitted (28-PRB-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (Dasse 1 to 213673)
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83170 ACAGCTTTAAAATTCAAATTTTCAAAAGATATCTATAACATCAGAAACTAAA 83119
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/organism="Mus musculus"
/orlarype="genomic DNA"
/db_xref="texton:10090"
/chromesome="18"
/clone="RP23-121N18"
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Unpublished
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Best Local Similarity 60.3<sup>5</sup>
Matches 140; Conservative
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                                                             RESULT 14
AC130218
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Rattus norvegicus clone CH230-63014, WORKING DRAFT SEQUENCE, 26
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Submitted (02-FBB-2003) Human Genome Sequencing Center, Departmen
Submitted (02-FBB-2003) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 117886)
Worley, K.C.
Direct Submission
                                                                                                                                                                  ACI39385.5 GI:30521076
HTG; HTGS_PHASE1; HTGS_DRAFT.
Rattus norvegicus (Norway rat)
Rattus norvegicus (Nordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 117886)
RESULT 15
AC139385/c
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DEFINITION
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AUTHORS
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KEYWORDS
SOURCE
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JOURNAL

COMMENT

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Submitted (10-MAY-2003) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:30466934.
Center: Baylor College of Medicine
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Center: Contact: May 10, 2003 this sequence version replaced gi:30466934.
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Center: Contact: Macchalp@bcm.tmc.edu/
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Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1368: contig of 1368 bp in length 1468: gap of unknown length 3011; contig of 1414) bp in length 3011; gap of unknown length 14181: contig of 1170 bp in length 4281; gap of unknown length 14281; gap of unknown length 5508: gap of unknown length 7746: contig of 1020 bp in length 7746: contig of 1020 bp in length 7746: contig of 1052 bp in length 1658: gap of unknown length 10064: contig of 1052 bp in length 10164; gap of unknown length 10164; gap of unknown length 11371; contig of 1050 bp in length 11371; contig of 1010 bp in length 14501: contig of 1011 bp in length 1539; gap of unknown length 16504; contig of 1011 bp in length 16394; gap of unknown length 16504; contig of 1033 bp in length 16504; contig of 1033 bp in length 16394; gap of unknown length 16394; gap of unknown length 16394; gap of unknown length 16394; gap of unknown length 13137; contig of 4405 bp in length 13137; contig of 4405 bp in length 13137; contig of 4405 bp in length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unknown length 17266; gap of unk
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Score	Match	Match Length DB	DB	Ωï	Description	A X X
1677	100.0	1677	9	ABV83605	Abv83605 Human bre	PA
647.2	38.6	667	9	ABV83604	Abv83604 Human bre	× _
554.8	33.1	3102	m	AAC75441	Aac75441 Human ORF	PI PI
420.2	25.1	1718	7	ADA53214	Ada53214 Human cod	Id.
108.6	6.5	1338	4	ABL29731	Abl29731 Drosophil	× _
108.6	6.5	6497	4	ABL29730	Ab129730 Drosophil	DR.
7 107.6	6.4	2822	۲	ABX71178	Abx71178 Novel hum	×
3 76.8	4.6	3316	4	ABL10742	Abl10742 Drosophil	Pq.
9 76.6	4.6	1817	ស	ABA15256	Aba15256 Human ner	
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1 75.2	4.5	710	v	ABT09598	Abt09598 Phase-1 R	× —
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3 73.6	4.4	2278	4	ABL12518	Abl12518 Drosophil	2
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19 73.2			9	ABS65032	Abs65032 Invertebr	<u>ნ</u>
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1 73	4.4	742	φ	ABS76748		<u></u>
2 72.6	4.3	338	Q	ADD19844	-	<u></u>
3 72.4	4.3	296	σ	ADD19952	Add19952 Oreochrom	ŏ _

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4 9 ADD20177 7 8 ADA37416 4 9 ADD37416 8 2 AARG6617 5 9 ADD20225 5 9 ADD20225 6 0 8 ADD20225 6 9 ADD19778 6 9 ADD19778 7 4 AARA34378 7 5 AARA34378 7 5 AARA34378 7 6 ABS02604 7 6 ABS02604 7 6 AARO2801	SEQ ID NO 48. cancer; transg 84. P, Recipon H,	nucleic nosing, no cancer i English read breast no coling a one of a one of a cleant of acid mole diagnosin on cancer tr
72.4 4.3 72.2 72.2 72.2 72.2 72.2 72.2 72.2 73.1 70.8 7	605 standard; 605; C-2002 (first breast specif ; breast; cytc ss. sapiens. 266605-A2. G-2002. 18-2002; 2002WG 18-2001; 2001US 19-) DIADEXUS IN	isolated breast ful for identifyi ating breast cand in 1; Page 171-17 invention relate prisible ABP66708). 80558-ABV836722), (d) a molecule breast specific useful for iden ating breast cand ating breast cand ating breast cand ating breast cand ating breast cand ating breast cand ating breast cand ating breast cand ating breast cand ating breast cand
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transgenic animals are useful as animal model systems used in elaborating the biological function of the polypeptides, studying conditions and/or disorders associated with aberrant expression and in screening for compounds effective in ameliorating the conditions. The polynucleotides are useful for gene therapy and in vaccines 88888888

Tun Apr 22 09:40:01 2004

TR-TO-0/0-070-#0.TIB

ខ្ល	are useful for gene therapy and in vaccines	
S	Sequence 1677 BP; 407 A; 456 C; 473 G; 341 T; 0 U; 0 Other;	
OME	uery Match Sest Local Similarity 100.0%; Pred. No. 0; Atches 1677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
ò	GAGTTGGGGGTGGCCAAGGCCCAAGGGCTTGGGCTTCAGCATCCGTGGGGGCTCGGA	
QQ	1 GAGTIGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	
ò	CACGCGTGGGCATCTACGTGTCTCTGGTCGAACCAGGCTCTCTAGCTGAGAAGGAAG	
QD	61 CACGGCGTGGGCATCTACGTGTCTCTGGTAGCAACCAGGCTCTGAGCTGAGAAGGAAG	
à	121 CTGCGGGTCGGGGCACCAGATTCTGCGCGTCAACGACAAATCCCTGGCCCGGGTGACCCAC 180	
ор	121 cracadarcadatreracadareadanaareceradeeceadareeceadareecead 180	
ò	181 GCGGAGGCCGTCAAGGCTCTGAAGGGCTCCAAGAAGCTGGTGCTGTGTGTACTCAGCA 240	
Д	181 GCGGAGGCCGTCAAGGCTCTGAAGGGCTCCAAGAAGCTGGTGTCTGTGTACTCAGCA 240	
δ	241 GGGCGCATCCCTGGGGGCTACGTCACCACCACCTGGGTGGACCCGCAGGC 300	
DP	241 GGGCGCATCCCTGGGGGCTACGTCACCACCACATCTACACCTGGGTGGACCCGCAGGGC 300	
δ	301 CGCAGCATCTCCCCACCTCGGCCTGCCCCAGGCCCAGGTGGTGCCCTGAGGCAGCAG 360	
Ωp	301 GGAGCATCTCCCCACCCTCGGGCCTCCCCAGGCCCCACGGTGCCCTGAGGCAGCAG 360	
ò	361 GAGGGTGACCGGAGGACCCCTGCACCTCCTGCAAGGAGGGATGAGAAAAAGGTGAAC 420	
qq	361 GAGGGTGACCGGAGGAGCACCCTGCACGCAGGAGGGGGATGAGAAAAAGGTGAAC 420	
ò	421 CTGGTGCTGGGGGGACGGCCGGTCCCTGGGCCTCACGATCCGTGGGGGGAGCTGAGTACGGC 480	
gg	CTGGG	
à	481 CITGGCATITACATCACTGGCGTGGACCCCAGGCTCTGAAGCCAGAAGGCAGCGGGCTCAAG 540	
q	481 CTTGGCATTTACATCACTGGCGTGGACCCCAGGCTCTGAAGGCAGCGGGCTCAAG 540	
ઠે	541 GITGGGGACCAGAITCTAGAAGIGAAIGGGCGGGAGCTITCICAACAICCTACACGACGAG 600	
a	541 GITGGGACCAGATICTAGAAGTGAATGGGCGGAGCTITCTCAACATCTTACACGACGACGAG 600	
ò	601 GCTGTCAGGCTGCTTAAGTCATCTCGGCACCTCATCCTGACAGGACGTCGGGAGG 660	
q	601 GCTGTCAGGCTGCTTAAGTCATCTCGGCACCTCATCCTGACAGTGAAGGACGTCGGGAGG 660	
ò	661 CIGCCCCAIGCCGCACCACIGIGGACGAGACCAAGIGGAGTCGCCAGIICCCCGGAICAGG 720	
q	661 CIGCCCCAIGCCCGCACCACIGIGGACGAGACCAAGIGGATCGCCCGGAICAGG 720	
ò	721 GAGACCATGGCGAACTCGGCCACGCTCTGCTCGCTCCAATCTCCAGACCCCA 780	
엄	721 GAGACCATGGCGAACTCGGCAGGTCTGGCCCACTCTGGCTCGAATCTCCAGACCCCA 780	
ò	781 GGGCCATTCTGAAAGCCAGTGATAGCTGCCTCCATCCTCCACCGCCCTGGCTCTCCT 840	
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1625

1566 AGACAAGACTAGAGAAAACACAGGACAGGGGCAAAACCACGTGAGGGAGCAACACAGA

Cafferkey R;

Karra K,

Recipon H,

Hu P,

us-10-078-090-48.rng

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The invention relates to human breast specific nucleic acids (I)

C comprising: (a) a sequence encoding any one of 95 protein sequences

C (ABV65614-ABP66708); (b) any one of 115 polymucleotide sequences

C (ABV6358-ABV83672); (c) a molecule that selectively hybridizes to (a) or

C (b); (d) a molecule having at least 60% sequence identity to (a) or (b).

The breast specific nucleic acid molecules, polymeptides and antibodies

CC The breast cancer and non-cancerous disease states in breast tissue.

CT reating breast cancer and non-cancerous disease states in breast tissue.

CT They are also useful for producing transgenic animals and cells and

CT producing engineered breast tissue for treatment and research. The

CT producing animals are useful as animal model systems used in elaborating

CT disorders associated with aberrant expression and in screening for

C compounds effective in ameliorating the conditions. The polymucleotides

C are useful for gene therapy and in vaccines
                                                                                                                                                                                                          New isolated breast specific nucleic acid molecules and polypeptides, useful for identifying, diagnosing, monitoring, staging, imaging and treating breast cancer and non-cancerous disease states in breast tissue.
                                                                                                                                                                                                                                                                                                               Claim 1; Page 170-171; 254pp; English.
15-FEB-2001; 2001US-0268999P
                                                                                             Salceda S, Macina RA,
Sun Y, Liu C;
                                                  (DIAD-) DIADEXUS INC
                                                                                                                                                                    WPI; 2002-713345/77.
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Sequence 667 BP; 201 A; 140 C; 178 G; 148 T; 0 U; 0 Other;

1145 TCATCCTATCATTACATAGTAGTATAATAATAATATTAGAGAGATACACAGAAAATATA 1445 TAGAGAAGATAACAGTGTTCTCTATAAAAAAAAAAAGCTGCCCTCTCTGGATAGCTTCT 1505 .. 0 1085 1205 1265 135 195 555 255 315 376 icarcciarcarracaracracianaraaraaraararracacacacacacacacaarara 435 75 TAGTTGCCAACAGTGTAATGTGTCACCTTTTGATCTTCATCAGAAATCTCAGGCTGGTGG TAGTTGCCAACAGTGTAATGTGTCACCTTTTGATCTTCATCACAAATCTCAGCTGGTGG 436 TAGAGAAGATAACAGTGTTCTCTATAAAAAAAAAAACAGCTGCCCTCTCTGCATAGCTTCT 16 GAGGICCATAACCCTGCCCTCATCCCAGATCTGTGCAGATGAAAGAAGAGAAGAGAAGAGA 1086 GAAAGAGAGATGCTTTGGGGTGTATTTGGCCAGAGGCCACCAGGCTGGATCCCATGAA GAAAGAGAGAGATGCTTTGGGGTGTATTTGGCCAGAGGCCACCAGGCTGGATCCCATGAA 1146 GAAATCTGGGTGAGAGGGTCTTAAAGTCATAAACTGAGATCCAGTTGCCAGGTGGCTGCA Gaps ô Query Match

38.6%; Score 647.2; DB 6; Length 667;

Best Local Similarity 99.5%; Pred. No. 1.8e-153;

Matches 649; Conservative 0; Mismatches 3; Indels 0; 1386 1206 196 1266 1326 16 256 316 1446 g 8 6 8 8 8 8 셤 g ò Б 8 엄 ઠે à

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which to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipartitic; antipartkinsonian; nootropic; neuroprotective; osteopathic; anticorvulsant; antiarthitic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; prypotensive; dermatological; immunosuppressive; antidiabetic; prypotensive; dermatological; immunosuppressive; antithyroid; antibacterial; nantivital; antifungal; antitheumatic; antithyroid; and antibacterial; to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative
                615
                                                                                                                                                                                                                                                                                                                                                                              Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticorulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antianatory; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; cancer; proliferative disorder; hypertension; neurodegenerative disorder; cancer; proliferative disorder; hypertension; neurodegenerative disorder; proliferative disorder; hypertension; neurodegenerative disorder; proliferative disorder; babs; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; severe combined immunodeficiency; malaria; autoimmuno disorder; aethma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; broom damage; cartilage damage; antiinflammatory disease; coagulation;
frame X,
                                                                                   616 GGGGGAACCACATTACCCCACACGTGAAAAAGGGAGACCAGGGGGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                             Human ORFX ORF996 polynucleotide sequence SEQ ID NO:1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 1517-1519; 5507pp; English.
                                                                1626 GGGGGGAACCACATTACCCCA
                                                                                                                                                                                                                  AAC75441 standard; cDNA; 3102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chrombosis; contraceptive; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-WAR-1999; 99US-0127607P.
02-APR-1999; 99US-0127636P.
05-APR-1999; 99US-0127728P.
30-WAR-2000; 2000US-00540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000WO-US008621.
                                                                                                                                                                                                                                                                                                      (first entry)
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disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mealitue, hypertrension, hypothyroidsm, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal hesmoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive
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                                                                                                                                                   Gaps
                                                                                                                                                0;
                                                                                                                       Score 554.8; DB 3; Length 3102;
Pred. No. 9e-130;
0; Mismatches 2; Indels 0;
                                                                                                Sequence 3102 BP; 699 A; 996 C; 860 G; 545 T; 0 U; 2 Other;
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                                                                                                                          Query Match
Best Local Similarity 99.6%;
Matches 556; Conservative
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New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.

Claim 1; SEQ ID NO 782; 205pp; English

H

Ishii S; R, Tamechika

Otsuki T, Wakamatsu A, Sato H, Hio Y, Otsuka K, Nagai K, Irie Otsuka M, Nagahari K, Masuho Y;

, Sugiyama T, J, Isono Y, F Yoshikawa T, (

Yamamoto J, Seki N, Y

WPI; 2003-395539/38. P-PSDB; ADA54853.

HELIX RES INST. RES ASSOC BIOTECHNOLOGY

(REAS-)

14-SEP-2001; 2001JP-00328381. 24-JAN-2002; 2002US-0350435P. 21-MAR-2002; 2002EP-00006586

19-MAR-2003

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                                                                                                                                                                                                                                                             The present invention relates to novel human secretory or membrane proteins (ADAS4072-ADAS5710) and their coding sequences (ADAS2433-ADAS4071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
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25.1%; Score 420.2; DB 7; Length 1718;
Best Local Similarity 95.0%; Pred. No. 9.1e-96;
Matches 434; Conservative 0; Mismatches 23; Indels 0;
                                                                                                                                                                                                                                                                                                                                  Sequence 1718 BP; 269 A; 611 C; 551 G; 287 T; 0 U; 0 Other;
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Thu Apr 22

ABL29730

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                           developmental biology; cell signalling; insecticide;
                                   Drosophila melanogaster genomic polynucleotide SEQ ID NO 40666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1338 BP; 303 A; 400 C; 384 G; 251 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                         1; SEQ ID NO 40666; 21pp + Sequence Listing; English.
                                                                                                                                                                                                               23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
                                                                                                                                                                                   23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid
genes from Drosophila and
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                                                                                                       Drosophila melanogaster.
                                                                               pharmaceutical; gene;
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            (first
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                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY
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interactions.
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            26-MAR-2002
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detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell

Myers EW,

PWD,

ó 507 GIGAACCIGGIGCIGGGGGACGGCCGGICCCIGGCCTCACGAICCGIGGGGAGCTGAG 474 534 raceecciessarcinnercacciscinaaraasacacscinscasicarccarccis 594 creardarrededadedadrecreadedreardededancerriciedareredadeded 447 TACGGCCTTGGCATTTACATCACTGGCGTGGACCCAGGCTCTGAAGCAGAAGGCAGCGGG CICAAGGITGGGGACCAGAITCIAGAAGIGAATGGGCGGAGCITTCICAACATCCIACAC GACGAGGCGGTGGGTTGAAGTACCACAAACGCATGTCGCTGGTGATACGTGACGTG Gaps .; 0 DB 4; Length 1338; dechaderideecehereerdendeneeneengangangeneerdeeneede Score 108.6; DB 4; Length Pred. No. 5.4e-17; 0; Mismatches 114; Indels 6.5%; Query Match
Best Local Similarity 60.8
Matches 177; Conservative ò

ABX71178 standard; cDNA; 2822

RESULT 6 ABL29730/c ID ABL29730 standard; DNA; 6497 BP. XX

4743 4803 4982 gradakacridarcakaccradrokarcradrorokadokardardarokardakadokadadada 4923 654 ŗ The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequence (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell GACGAGGCTGTCAGGCTGCTTAAGTCATCTCGGCACCTCATCCTGACAGTGAAGGACGTC 1802 gaccadececircecircaciricaachacecenaaccearcicercercaracercarcarcercare 415 GIGAACCIGGIGCIGGGGAACGGCCGGICCCIGGGCCTCACGAICCGIGGGGAGCTGAG 475 TACGGCCTTGGCATTTACATCACTGGCGTGGACCCCAGGCTCTGAAGCAGAAGGCAGCGGG CTCAAGGTTGGGGACCAGATTCTAGAAGTGAATGGGCGGAGCTTTCTCAACATCCTACAC choandarhdecdacdadantcchcdaddadhaddedcancchhichcdandheacedad ecchaecrececentecrecrecrecareandangeseceradoreced Sequence 6497 BP; 1933 A; 1221 C; 1417 G; 1926 T; 0 U; 0 Other; developmental biology; cell signalling; insecticide; DB 4; Length 6497; GGGAGGCTGCCCCATGCCCGCACTGTGGACGAGGACCAAGTGGATCGCC SEQ ID NO 40663; 21pp + Sequence Listing; English. 6.5%; Score 108.6; DB 4; Length 60.8%; Pred. No. 1.1e-16; Live 0; Mismatches 114; Indels Drosophila melanogaster genomic polynucleotide Myers EW PWD, 23-MAR-2001; 2001WO-US009231. 23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150. Query Match Best Local Similarity 60.87 Matches 177; Conservative (first entry) 금 Drosophila melanogaster pharmaceutical; gene; Adams M, WPI; 2001-656860/75 (PEKE) PE CORP WO200171042-A2. interactions. 26-MAR-2002 27-SEP-2001 Venter JC, 535 4862 4742 595 655 엄 엄 ò 원 ò 셤 ò ò

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(first entry) 05-MAR-2003

ABX71178;

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Gaps

39;

Mismatches 324; Indels

. 0

361; Conservative

Matches

000-010-01-01

Novel human cDNA sequence #403.

Human; gene; ss; nervous system disorder; peripheral neuropathy; huntington's disease; amyotrophic lateral sclerosis; haemophilia; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; nutoidmune disease; systemic lupus erythematosus; rheumacoid arthritis; insulin-dependent diabetes mellitus; anaemia; thrombocytopaenia; wound; ulcer; burn; bone disorder; osteoprosis; osteoarthritis; stroke; fibrosis; reperfusion injury; infection; allergic rhinitis; asthma; coagulation disorder; cancer; tumour; inflammatory disease; septic shock; differentiation; stem cell growth factor; haematopoiseis; chemokinetic; haemostatic; antinflammatory; expressed sequence tag; EST.

Homo sapiens

WO200281731-A2.

17-OCT-2002

9-JAN-2002; 2002WO-US001222

30-JAN-2001; 2001US-00774528

(HYSE-) HYSEQ INC. (GOOD/) GOODRICH R W.

Zhao QA, Ren F; Drmanac RT; Zhang J, Wang D, Asundi V, F, Wang J, Tang TY, Liu C, Zhou P, Asu Xue AJ, Yang Y, Wehrman T,

WPI; 2003-058563/05.

Novel polypeptide useful for treating neurodegenerative diseases, myeloid or lymphoid dell disorders, bone disorders, mechanical and traumatic disorders, coagulation disorders, and inflammatory diseases.

Claim 1; Page; 612pp; English.

This invention relates to the cDNA sequences encoding an isolated novel human polypeptide. The protein encoded by the nucleic acid of the convention is useful for treating central and peripheral nervous system diseases (e.g. peripheral neuropathy, Huntington's disease, amyotrophic clateral scleroats); neurodegenerative disease (e.g. Parkinson's disease, anyotrophic clateral scleroats); neurodegenerative disease (e.g. Parkinson's disease, anyotrophic clateral scleroats, rheumatoid arthritis, insulin-dependent diabetes mellitus) crancers, burns; bone disorders (e.g. systemic lugus clateral); nechanical and traumatic disorders (e.g. stroke, head trauma); lung or liver fibrosis; reperfusion injury in various tissues; osteoarthritis); asthma; coagulation disorders (e.g. septic shock, crancer and tumours; and inflammatory diseases (e.g. septic shock, Crohn's disease, anaphylaxis). The protein may be used to inhibit the growth, crifection or function of infectious agents such as bacteria, fungi, viruses, or to effect bodily characteristics, biorhythms or circadian cycles of rhythms. The protein may also have cycles of rhythms. The protein may also have creating, immune stimulating or suppressing, chemotactic/chemokinetic, haemostatic and thrombolytic, receptor/ligand, and antinflammatory crecumbinant protein for analysis. The present sequence represents a novel human cDNA sequence of the invention, this sequence is an expressed cycle sequence tag (EST) and was identified using subtractive hybridisation.

Sequence 2822 BP; 557 A; 893 C; 922 G; 450 T; 0 U; 0 Other;

Drosophila melanogaster.

WO200171042-A2

27-SEP-2001

6.4%; Score 107.6; DB 7; Length 2822; 49.9%; Pred. No. 1.4e-16; Query Match Best Local Similarity

564 848 684 444 504 264 587 324 647 325 CTGCCCCAGCCCCACGGTGGTGCCCTGAGGCAGCAGGAGGGTGACCGGAGGAGCACCCTG 384 728 144 467 204 648 ggrrchacaccci----dacaccadcrcagaadarddrordddddardrordd 701 84 GACCATGGTGGCTGGCCGAGGAGATGGCATCAAGGTGGGGGACCAGGTCCTGGCAGCC sza adcagcadcegechdeacandangdhegecegengddecegengecegegearcaagnic CTATAC-----ACAACCTCCGACGACTTCTGC GACCCAGGCTCTGAAGCAGAAGGCAGCGGGCTCAAGGTTGGGGACCAGATTCTAGAAGTG 849 AACGGTGTCAGGTTTGACGACATCAGCCACAGGCCGTGGAGGTGCTGAAGGGCCAA 685 GACGAGACCAAGTGGATCGCCAGTTCCCGGATCAGGGAGACCATGGCGAACTCGGCAGGG 265 ACCAACCACATCTACACCTGGGTGGACCCGCAGGCCGCAGCATCTCCCCCACCCTCGGGC CTGGGCCTCACGATCCGTGGGGGGCTGAGTACGGCCTTGGCATTTACATCACTGGCGTG cresecricaacarceresesesesaseaacirrasecresecarcrarerereaasere 565 AATGGGCGGAGCTTTCTCAACATCCTACACGAGGCTGTCAGGCTGCTTAAGTCATCT CGGCACCTCATCCTGACAGTGAAGGACGTCGGGAGGCTGCCCCATGCCCGCACCACTGTG 909 ACGCACATCATGCTGACCATCAAGGAGACCGGCCGGTATCCTGCCTACAAGGAGATGGTT 145 CGCGTCAACGACAAATCCCTGGCCCGGGTGACCCACGCGGAGGCCGTCAAGGCTCTGAAG CACCTCCTGCAAGGAGGGATGAAAAAGGTGAACCTGGTGCTGGGGGACGGCCGGTCC 85 CTGGTGGAACCAGGCTCTCTAGCTGAGAAGGAAGGACTGCGGGGTCGGGGACCAGATTCTG 108 AAAGTGGAGGAAAGGCAGCAGTGCAGAGCGGGCTGGCCTGCGTGGGGGGGAAAGATCACG 205 GGCTCCAAGAAGCTGGTGTGTGTGTACTCAGCAGGGCGCATCCCTGGGGGCTACGTC 25 GAGGGCTTGGGCTTCAGCATCCGTGGGGGCTCGGAGCACGGCGTGGGCATCTACGTGTT developmental biology; cell signalling; insecticide; Drosophila melanogaster expressed polynucleotide SEQ ID ABL10742 standard; cDNA; 3316 BP. (first entry) pharmaceutical; gene; ss |||| |TCTG 1032 745 TCTG 748 26-MAR-2002 Drosophila; ABL10742; 385 702 729 505 789 445 ద ď d $\stackrel{>}{\circ}$ 9 9 9 8 6 ò d à DP 8 6 à ò ò à ò ð d 6

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24 - FEB - 2000; 2000US - 0184664P.

16 - MAR - 2000; 2000US - 0189550P.

16 - MAR - 2000; 2000US - 0189574P.

17 - MAR - 2000; 2000US - 0198123P.

18 - MAY - 2000; 2000US - 0198123P.

19 - MAY - 2000; 2000US - 0209467P.

20 - JUL - 2000; 2000US - 0214886P.

30 - JUL - 2000; 2000US - 0214886P.

31 - JUL - 2000; 2000US - 0214886P.

32 - JUL - 2000; 2000US - 0214886P.

33 - JUL - 2000; 2000US - 0214886P.

34 - JUL - 2000; 2000US - 0214886P.

35 - JUL - 2000; 2000US - 0214886P.

36 - JUL - 2000; 2000US - 0214886P.

37 - JUL - 2000; 2000US - 0214886P.

38 - JUL - 2000; 2000US - 0214886P.

39 - JUL - 2000; 2000US - 0214886P.

44 - JUL - 2000; 2000US - 0214886P.

44 - JUL - 2000; 2000US - 021489P.

44 - JUL - 2000; 2000US - 021489P.

44 - JUL - 2000; 2000US - 0225244P.

44 - JUL - 2000; 2000US - 0225244P.

44 - JUL - 2000; 2000US - 0225244P.

44 - JUL - 2000; 2000US - 0225244P.

44 - JUL - 2000; 2000US - 0225244P.

45 - JUL - 2000; 2000US - 0225244P.

46 - JUL - 2000; 2000US - 0225244P.

47 - JUL - 2000; 2000US - 0225244P.

48 - JUL - 2000; 2000US - 0225244P.

49 - JUL - 2000; 2000US - 0225244P.

40 - 2000; 2000US - 0225244P.

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40 - 2000; 2000US - 0225268P.

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41 - 2000; 2000US - 0225268P.

42 - 2000; 2000US - 0225268P.

43 - 2000; 2000US - 022528P.

44 - 2000; 2000US - 022528P.

45 - 2000; 2000US - 022528P.

46 - 2000; 2000US - 022528P.

47 - 2000; 2000US - 022528P.

48 - 2000; 2000US - 022528P.

49 - 2000; 2000US - 022528P.

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41 - 2000; 2000US - 022528P.

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46 - 2000; 2000US - 022
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        CARGICIGICIGICIGICIGICIGICICICICICIGIGIGICICIGIGIGIGIGIGICIGICICICI 1350
                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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4.6%; Score 76.8; DB 4; Length 3316;
Best Local Similarity 87.5%; Pred. No. 9.3e-09;
Matches 84; Conservative 0; Mismatches 12; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3316 BP; 751 A; 787 C; 708 G; 1070 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 26708; 21pp + Sequence Listing; English.
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2000US-0180628P.
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                                                      23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                           23-MAR-2001; 2001WO-US009231
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                                                                                                                                         Venter JC, Adams M,
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                                                                                                        (PEKE ) PE CORP NY
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04-FEB-2000;
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Thu Apr 22 09:46:01 2004
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17-NOV-2000; 2000US-0249209F.
17-NOV-2000; 2000US-0249210F.
17-NOV-2000; 2000US-0249210F.
17-NOV-2000; 2000US-02492118F.
17-NOV-2000; 2000US-0249213F.
17-NOV-2000; 2000US-0249213F.
17-NOV-2000; 2000US-0249218F.
17-NOV-2000; 2000US-0249218F.
17-NOV-2000; 2000US-0249218F.
17-NOV-2000; 2000US-0249218F.
17-NOV-2000; 2000US-0249218F.
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17-NOV-2000; 2000US-0249218F.
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17-NOV-2000; 2000US-0249218F.
17-NOV-2000; 2000US-025118F.
17-NOV-2000; 2000US-025118F.
18-DEC-2000; 2000US-025118F.
18-DEC-2000; 2000US-025188F.
18-DEC-2000; 2000US-025188F.
18-DEC-2000; 2000US-025188F.
18-DEC-2000; 2000US-025188F.
18-DEC-2000; 2000US-025188F.
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20-OCT - 2000; 2000US-0241808P.
20-OCT - 2000; 2000US-0241808P.
20-OCT - 2000; 2000US-0241828P.
20-OCT - 2000; 2000US-0244617P.
08-NOV-2000; 2000US-0246414P.
08-NOV-2000; 2000US-0246478P.
08-NOV-2000; 2000US-0246478P.
08-NOV-2000; 2000US-0246478P.
08-NOV-2000; 2000US-024652P.
08-NOV-2000; 2000US-024652P.
08-NOV-2000; 2000US-024652P.
08-NOV-2000; 2000US-024652P.
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08-NOV-2000; 2000US-024651P.
08-NOV-2000; 2000US-024661P.
08-NOV-2000; 2000US-024661P.
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08-NOV-2000; 2000US-024661P.
08-NOV-2000; 2000US-024661P.
08-NOV-2000; 2000US-024661P.
002-0CH-2000; 20-0CH-2000; 20-0
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(HUMA-) HUMAN GENOME SCI INC

Ruben SM Rosen CA, Barash SC, Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.

Disclosure, SEQ ID NO 7587; 1701pp + Sequence Listing; English

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The invention relates to novel genes (ABA11004-ABA21534) and proteins coefficiens e.g. by protein or gene therapy. The genes are medical conditions e.g. by protein or gene therapy. The genes are medical conditions e.g. by protein or gene therapy. The genes are coefficient or genes are an edge of human tissues disclosed in the specification.

The nucleic acids, proteins, antibodies and (ant) agonists are useful in the nucleic acids, treatment and prevention of: (a) cancer, e.g. breast and covarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune constructions of discase, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's discase, cardiovascular discrders such as myocardial isohaemias; (d) wound healing conditions diseases such as viral, bacterial inchaemias, (d) wound healing confections diseases e.g. cerebral anoxia and parasitic confections diseases e.g. cerebral anoxia and epilepsy; and (f) infections diseases such as viral, bacterial, fungal and parasitic confections. Note: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly conference of the princed specification, but was obtained in electronic format directly conference and parasity.
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4.6%; Score 76.6; DB 5; Length 181
Best Local Similarity 64.2%; Pred. No. 7.9e-09;
Matches 115; Conservative 0; Mismatches 64; Indels
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RESULT 10 ADD25213/c

ADD25213 standard; DNA; 271990 ADD25213;

15-JAN-2004 (first entry)

Fertility restorer protein genomic DNA sequence.

fertility restorer protein, male sterile plant; viable pollen production; selection marker; ds; gene.

Unidentified.

WO2003006622-A2.

23-JAN-2003

12-JUL-2002; 2002WO-US022217.

12-JUL-2001; 2001US-0305026P. 13-JUL-2001; 2001US-0305363P. 30-JUL-2001; 2001US-0308736P.

(UYMC-) UNIV MCGILL. (DNAL-) DNA LANDMARKS INC.

Jin Cheung W, Landry BS, Brown GG, Formanova N, Dendy C,

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WPI; 2003-221734/21

New nuclear fertility restorer genes, useful for restoring fertility in cytoplasmic male-sterile plants such as Brassica napus plants, or for increasing production of viable pollen in a plant.

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The invention relates to a method used for evaluating the toxicity of an agent comprising determining the expression of a rat toxic response grent(s) in the test animal in response to the agent. The method is useful in drug development, particularly for conducting toxicity studies and analysis before a new drug or compound is approved for human consumption
                                                                                                                                                                                                                                                                                                                         1348 GTGTGTGTGTGTGTGTGTGTGTCTCCTCACTCTTTCATCCTATCATTACATAGTAG 1407
                                              The invention comprises the amino acid and coding sequences of isolated fertility restorer proteins. The DNA and protein sequences of the invention are useful for restoring fertility in male sterile plants, such as Brassica napus plants. The DNA and protein sequences of the invention are useful for increasing production of viable pollen in a plant. The DNA and protein sequences are also useful as selection markers to identify transformed plant cells. The present genomic DNA sequence contains coding sequences for fertility restorer proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evaluating the toxicity of an agent, useful in drug development or in determining toxicological responses to a new drug, by determining the expression of rat toxicologically relevant genes in the test animal in response to the test agent.
                                                                                                                                                                                                               Other;
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                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83121 TATTAAACTGAATCTAATTTAATGTGTGTATATATATAATATATAATTA 83072
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                                                                                                                                                                                                                 Seguence 271990 BP; 89597 A; 47325 C; 46930 G; 88078 T; 0 U; 60
                                                                                                                                                                                                                                                Query Match

4.5%; Score 75.6; DB 9; Length 271990;
Best Local Similarity 65.3%; Pred. No. 1.5e-07;
Matches 111; Conservative 0; Mismatches 59; Indels 0;
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                 SEQ ID NO 87; 191pp; English.
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26-JUL-2001; 2001US-0308161P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                 Claim 1;
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ABT09598/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is the coding sequence for human PDZ protein 20. PDZ protein 20 and its coding sequence are useful in the diagnosis and treatment of malignant tumour, haemopathy, HIV infection, immunological diseases and various inflammations
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or use. The method is also useful in determining toxicological responses to a new drug. This polynucleotide sequence represents a phase-1 rat CT gene of the invention
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4.4%; Score 73.8; DB 4; Length 1274;
Best Local Similarity 55.2%; Pred. No. 3.4e-08;
Matches 144; Conservative 0; Mismatches 117; Indels 0;
                                                                                           Length 710;
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                                                                Sequence 710 BP; 218 A; 148 C; 189 G; 150 T; 0 U; 5 Other;
                                                                                         4.5%; Score 75.2; DB 6; Length 774.2%; Pred. No. 1.1e-08; vative 0; Mismatches 33; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PDZ protein 20 coding sequence
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                                                                                                                                                                                                                                                                                                                                                                       AAH73917 standard; cDNA; 1274 BP
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nes 95; Conservative
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P-PSDB; AAG64378.
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                                                                                               Query Match
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AAH73917
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA aequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                 634
                                                                  144
                                                                                                                                                                                                                                                635 GAGGTGAATGGGCTGAGCCTGGAGACACCACCATGGGTAGGCTGAAAGGTGCTGACC 694
                                                                                                                                                                                                                                                                                                                                            205 GCTCCAAGAAGCTGGTGTGTGTGTACTCAGCAGGGCGCATCCCTGGGGGCTACGTC 264
                                                                                                                                                                                                                                                                                                                                                                                                               695 Accadedacedecriceaeardarderredeceartedecedardredecedecarcaagric 754
                                                                                                                                                                                                       CGCGTCAACGACAAATCCCTGGCCCGGGTGACCCCACGCGGAGGCCGTCAAGGCTCTGAAG 204
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                                                                                                                                 575 AAAGITGGAGGAAGGCAGCAGTGCAGAGCGGGCTGGCCTGTGCGTGGGGGACAAGAICACG
GGGAGGCTTGGGCGTGCGCGGGGGCTCAGAGCATGGCCTGGGCATCTTCGTCAGC
                                                                  CTGGTGGAACCAGGCTCTCTAGCTGAGAAGGAAGGACTGCGGGGTCGGGGACCAGATTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster expressed polynucleotide SEQ ID NO 32036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila, developmental biology, cell signalling, insecticide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.4%; Score 73.6; DB 4; Length 2278; 71.3%; Pred. No. 5e-08; 1.1.0 0; Mismatches 39; Indels 0
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ABL12518 standard; cDNA; 2278 BP
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11-JUL-2000; 2000US-00614150.
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The present invention describes an isolated nucleic acid (I) comprising a single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of Salmo salar SNPs, concokronism injoricus SNPs or Atlantic halibut SNPs; cand (ii) a nucleic acid having nucleotide sequence that hybridises to complement under highly stringent hybridisation conditions. Also described: (I) an isolated objoundleotide (II) comprising at least I contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O. niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod polymorphic sites and seabass polymorphic sites, or thear complement; (2) a primer pair (III) suitable for use in PCR, comprising two (II) capable of amplifying a nucleotide sequence chosen from S. salar SNPs and, O. or niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod polymorphic sites and seabass polymorphic sites, or thear complement; (2) applymorphic sites and seabass polymorphic sites, and determining (MI) the origin of fish sample comprising providing a parentage genotype database complements a distinct origin, and comparing a sample genotype to the parentage genotype database, where a match between condidate parent genotype to the parentage genotype database, where a match between condidate parent genotype identifies to the sample genotype and one of the candidate parent genotype identifies to the origin of the sample such as family salmonidae, S. salar, Tilapia, O. niloticus, rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid molecule comprising single nucleotide polymorphism associated with fish, useful for forming PCR primers which are used for detecting single nucleotide polymorphisms in fish nucleic
                                                                                                                                                                                     single nucleotide polymorphism; SNP; fish, Salmo salar; Orechromis niloticus; Atlantic halibut; microsatellite; cod; polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut; detection; gene; ds.
                                                                                                                                                                 Seabass polymorphic site nucleotide sequence SEQ ID NO:433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 32; SEQ ID NO 433; 233pp; English
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16-AUG-2002; 2002US-0404200P.
                                    ADD19798 standard; DNA; 667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENO-) GENOMAR ASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Slettan A,
                                                                                                                                                                                                                                                                                                                                                               WO2003060160-A2.
                                                                                                                            15-JAN-2004
                                                                                                                                                                                                                                                                                                                      unidentified
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ö detecting nucleic acid molecule comprising SNP in a sample, which involves contacting the sample containing nucleic acids with one or more involves contacting the sample containing nucleic acid who in injuricus SNPs, and identifying nucleic acid that hybridises to (II). (II) is useful for detecting nucleic acid molecule comprising a polymorphic sequence in a sample, comprising the sample containing nucleic acids with one or more (II) which is derived from 0. miloticus microsatellite, 0. miloticus SNPs, Atlantic halibut SNPs, cod polymorphic sites or seabass polymorphic sites, and identifying a nucleic acid that hybridises to (II) (III) is useful for detecting nucleic acid molecule comprising a microsatellite sequence in sample. The present sequence is used in the exemplification of the present invention. 169 didididididididididididididilarechaangeacannagegginahnaaraagn 110 0; Gaps Length 667; Query Match

4.4%; Score 73.4; DB 9; Length 66'
Best Local Similarity 68.7%; Pred. No. 3.2e-08;
Matches 101; Conservative 0; Mismatches 46; Indels Sequence 667 BP; 207 A; 185 C; 102 G; 167 T; 0 U; 6 Other; 1408 TATAATAATAATATAGAGAGATACA 1434 83 109 AATAACCCTAACGAGAAGAGAGGGACA 88666666666668888 g ð g ð ò

Mouse Itk carcinoma associated gene, SEQ ID NO:1319. ADA02801 standard; DNA; 67832 BP (first entry) 06-NOV-2003 ADA02801

Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening; gene; da

WO2003057146-A2 Mus sp.

26-DEC-2002; 2002WO-US041414

17-JUL-2003

26-DEC-2001; 2001US-00035832

(SAGR-) SAGRES DISCOVERY

Morris DW;

WPI; 2003-587068/55

New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.

The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a CA nucleic acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a biochip comprising CA nucleic acid or Claim 1; SEQ ID NO 1319; 245pp; English

fragments thereof. The sequences of the invention were identified using oncogenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protoconcogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (sepecially breast cancer, prostate cancer, lymphoma or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular cissues. CA nucleic acids, proteins and antibodies are also useful as therapeutic agents and in screening and evaluating drug candidates. The present sequence represents a specifically claimed murine CA nucleic acid sequence of the invention. Note: The complete sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the print of the printed specification, but was obtained the winted pot_sequences. ò Sequence 67832 BP; 17054 A; 15504 C; 15824 G; 18278 T; 0 U; 1172 Other; Gaps . 0 Length 67832; 16; Indels 61764 Grenererererererererererarerracereaaacter 61802 1348 grandrardrardrardrardrarcracycoccutr 1386 y Match
Local Similarity 83.8%; Pred. No. 2.8e-07;
hes 83; Conservative 0; Mismatches 16; Query Match g 8888888888888888888888 8 à

Search completed: April 21, 2004, 21:36:02 Job time : 654.769 secs

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April 21, 2004, 19:28:36 ; Search time 6476.91 Seconds (without alignments) 11222.365 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	AL138895 Human DNA AR336382 Homo sapi AR040959 Homo sapi AR122523 Mus muscu AY227205 Rattus no AL110228 Homo sapi AX714098 Sequence AX056190 Homo sapi AX714098 Sequence AX056190 Homo sapi AC127863 Rattus no AL683828 Muse DNA AR336379 Mus muscu AC015144 Drosophil AC010699 Drosophil AC02967 Homo sapi AC119686 Danio rer BX66474 Danio rer BX66474 Danio rer BX606295 Danio rer BX66474 Danio rer BX61101 Danio rer BX61101 Danio rer BX68695 Zebrafish BX68695 Zebrafish BX686992 Danio rer AC13187 Mus muscu BX68685 Zebrafish BX686992 Danio rer AC131587 Mus muscu BX088685 Zebrafish BX686992 Danio rer AC131587 Mus muscu BX088685 Zebrafish BX686992 Danio rer AC131587 Mus muscu BX088685 Zebrafish BX686992 Zebrafish BX68690 Zebrafish AC129157 Mus muscu	linear PRI 27-JUN-2001 on chromosome 9, complete Vertebrata; Buteleostomi;
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note="MIR repeat: matches 52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Lns9
RP11-9M16 is from the library RPCI-11.1 constructed by the group of pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-9M16 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true right end of clone RP11-9M16 is at 132322 in this sequence. The true left end of clone RP11-9M23323 in this sequence. The true left end of clone RP11-9M23323 is at 124695 in this sequence.
Submitted (27-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonereques@sanger.ac.uk
On Jun 28, 2001 this sequence version replaced gi:14456172.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Emi. EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP than the langer of the property of the langer on the found at the langer of the longer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the langer of the

    .301
note="LIMC1 repeat: matches 5718. .5955 of consensus"

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note="MER63A repeat: matches 46. .206 of consensus"
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note="AluSq repeat: matches 1. .298 of consensus"
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note="MIR repeat: matches 115. .166 of consensus"
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note="MIR repeat: matches 79. .165 of consensus"
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note="MIR repeat: matches 49. .142 of consensus"
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note="AluSc repeat: matches 5.
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/db_xref="taxon:9606"
/chromecome="9"
/clone="RP11-9M16"
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note="CpG island"
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/note="MIR re
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note="L2 re
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note="MIR repeat: matches 34. .144 of consensus" 20542. .20994 note="Charlie4a repeat: matches 26. .506 of consensus" 1034. .8179 'note="LTR16A repeat: matches 200. .354 of consensus" 1160. .8271 'note="LTR16C repeat: matches 255. .368 of consensus" .0037. .10131 'note="12 repeat: matches 2167, .2289 of consensus" 10460. .30627 21421. .21521 /note="12 repeat: matches 2045. .2158 of consensus" 21523. .21758 9523. .29664 note="L2 repeat: matches 2593. .2734 of consensus" intering repeat: matches 2372. .2688 of consensus" 6113. .16847 .2709 of consensus" .2674 of consensus" /note≈"MER5B repeat: matches 1. .173 of consensus" note="MIT2CB repeat: matches 1. .492 of consensus" 15702. .15995 note="L2 repeat: matches 2405. .2521 of consensus" 1151. .11327 .2707 of consensus" .254 of consensus" .298 of consensus" .232 of consensus" /note="MIR repeat: matches 28. .153 of consensus" 26919. .27000 /note="MIR repeat: matches 64. .147 of consensus" 27292. .27435 note="WIR repeat: matches 16. .262 of consensus" 5889. .26233 .140 of consensus" yss. ./*s/ note="MLT1D repeat: matches 3. .503 of consensus" consensus, .230 of consensus" note="MSTA repeat: matches 1. .426 of consensus" 3319. .23495 2339. .23495 7note="MIR repeat: matches 5. .192 of consensus" 24438. .24542 7note="MIR repeat: matches 28. .140 of consensus" 24993. .25526 note="MIR repeat: matches 23. .241 of consensus" 8972. .19080 note="MIR repeat: matches 18. .205 of consensus" (1579. .11883 note="MIR_repeat: matches 80, .258 of consensus" 4071, .14205 note="MIR repeat: matches 92. .226 of consensus" 5216. .15653 note="MIR repeat: matches 14. .123 of consensus" 0604: .10711 .181 of consensus" note="WIR repeat: matches 97. .243 of consensus" 2598. .12717 .144 of consensus" conserved" note="AluSx repeat: matches 1. .304 of .1886. .12024 note="L2 repeat: matches 1940. 16875. 16922 note="12 copies 4 mer atga 81% 7482. .17573 hote="L2 repeat: matches 2099. |5630. .25867 'note="AluJo repeat: matches 1. (2863. .23243 note="L2 repeat: matches 2363. note="MIR repeat: matches 102. note="AluSx repeat: matches 1. 'note="MIR repeat: matches 125. 8163. .18379 note="MIR repeat: matches 17.

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region region region region region region region region region region		146 of consensu. 15. Length 132292 15. Indels 0; CTTTCTCAACATCCTAC CTTTCTCAACATCCTAC CTTTCTCAACATCCTAC CTGAACATCGCAGGGC CGGAACGCCAGGGCC GTGGATCGCCAGGCCC GTGGATCGCCAGTTCCCC	32803 GGTGCCCGCGCCCCACTGTGCACGACTGCACTGGCACTTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTTCCCACTTCCACTTCCACTTCCACTTCCACTTCCACTTCCACTTCCACTTCCACTTCCACTTCCACTTCCACTTCCACTTCCACTTCTCACTTCCATTCTCAAAGCCATTCTCAATAGCTCACTTCCACTTCCACTCCCACTCCATTCTCAAAAGCCACTTCTAATAGCTACTCCATTCCATTCCACTCCCACTCCATTCTCAATAGCTACTTCCATTCACTCCACTCCACTCCACTTCTCATTCAAAATACACTCAATAGCTACACTCAATAGCTACTTCACTTCACTTCACTTCAAAAAAAA

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Chara, O., Nagase, T. and Kikuno, R.
Direct Submission

Submitted (04-APR-2000) Osamu Ohara, Kazusa DNA Research Institute,
Department of Human Gene Research, 1532-3, Yana, Kisarazu, Chiba
292-0812, Japan (B-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913,
                                                                                                                                                                                                                                                                                                                           PRI 22-FEB-2001
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagase_T., Kikuno,R., Ishikawa,K., Hirosawa,M. and Ohara,O. Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro DNA Res. 7 (2), 143-150 (2000)
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                                                                                          ABO40959 3566 bp mRNA linear Phomo sapiens mRNA for KIAA1526 protein, partial cds. ABO40959
SK plus"
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llarity 99.9%; Pred. No. 1e-161;
Conservative 0; Mismatches 1;
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'gene="KIAA1526"
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8	596	TTGCGGCGTGCCAAGGCCCACGAGGGCTTGGGCTTCAGCATCCGTGGGGGCTCGGAGCAC 655
8	64	GGCGTGGGCATCTACGTGTCTCTGGTGGAACCAGGCTCTCTAGCTGAGAAGGACTG 123
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λ	124	CGGGTCGGGGACAGATTCTGCGCGTCAACGACAAATCCCTGGCCGGGTGACCCACGCG 183
ΩĐ	716	CGGGTCGGGGGACCAGATTCTGCGCGTCAACGACAAATCCCTGGCCCGGGTGACCCACGCG 775
οχ	184	GAGGCCGTCAAGGCTCTGAAGGCTCCTAAGAAGCTGGTGCTGTCTGT
Db	776	GAGGCCGTCAAGGCTCTGAAGGCTCCAAGAAGCTGGTGTTGTTGTGTACTCAGCAGGG 835
ò	244	CGCATCCCTGGGGGCTACGTCACCAACCACATCTACACCTGGGTGGACCCGCAGGGCCGC 303
qq	836	GCATCCCTGGGGGCTACGTCACCACCACCACCTGGGTGGG
δ	304	AGCATCTCCCCACCCTCGGGCCTGCCCCACGGTGGTGCTGCCTGAGCAGCAGAG 363
QQ	896	AGCATCTCCCCACCCTCGGGCCTGCCCAGCCCCAGGTGGTGCTCCTGAGGCAGGAGGAG 955
λ	364	GGTGACCGGAGGAGCACCTGCAAGGAGGGGATGAGAAAAAGGTGAACCTG 423
Db Db	956	GGTGACCGGAGGAGCACCTGCTCTGCAAGGAGGGATGAGAAAAAGGTGAACTG 1015
٥٧	424	GIGCIGGGGGACGGCCGGTCCCTGGGCCTCACGATCCGTGGGGGGAGCTGAGTACGGCCTT 483
qq	1016	GIGCIGGGGGGCCGGTCCCTGGGCCTCACGATCGGGGGAGCTGAGTACGGCCTT 1075
δχ	484	GGCATTTACATCACTGGCGTGGACCCCAGGCTCTGAAGCAGAGAGGCAGCGGGCTCAAGGTT 543
qq	1076	GCCATTTACATCACTGGCGTGGACCCAGGCTCTGAAGCAGAAGGCAGCGGGCTCAAGGTT 1135
ò	544	GGGGACCAGATTCTAGAAGTGAATGGGCGGAGCTTTCTCAACATCCTACACGACGAGGCT 603
Db	1136	GGGGACCAGATTCTAGAAGTGAATGGGCGGGAGCTTTCTCAACATCCTACACGACGAGGCT 1195
ò	604	GTCAGGCTGCTTAAGTCATCTCGGCACCTCATCCTGACAGGAAGGTCGGGAGGCTG 663
Dβ	1196	GICAGGCTGCTTAAGTCATCTCGGCACCTCATCCTGACGAGGACGTCGAGGACGCTG 1255
λ̈́o	664	CCCCATGCCCGCACCACTGTGGACGAGCCAAGTGGATCGCCAGTTCCCGGATCAGGGAG 723
οp	1256	CCCCATGCCCGCACCACTGTGGACGAAGCAAGTGGATCGCCACGTTCCCGGATCAGGGAG 1315
٥٧	724	724 ACCAIGGCGAACTCGGCAGGTCT 747
Д	1316	ACCATGGCGAACTCGGCAGGGTTT 1339

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. AK122523 3178 bp mRNA Mus musculus mRNA for mKIAA1526 protein. AK122523 AK122523.1 GI:28972777 FLI_CDNA. Mus musculus (house mouse) Mus musculus DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM AK122523

l Okazaki, N., Kikuno, R., Ohara, R., Inamoto, S., Aizawa, H., Yuasa, S., Okazaki, D., Nagaee, T., Ohara, O. and Koga, H.
Prediction of the coding sequences of mouse homologues of KIAA, gene. II. The complete nucleotide sequences of 400 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries DNA Res. 10, 35-48 (2003) REFERENCE AUTHORS TITLE

REFERENCE

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Direct Submission
Submitted (07-FEB-2003) Hisashi Koga, Karusa DNA Research
Institute, Laboratory for Genome Informatics; 2-6-7

Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail:mouseGakausa.or.jp, Tel:81-438-52-3918)
The CREATE program supported by Japan science and technology
orporation; cDNA full insert sequencing: Kazusa DNA Research
Institute; cDNA library construction, clone selection and 5'- &
1. -3178 /dev_stage="adult" /note="vector:modified pBC SK+" 1. .3178 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="mbh03417" /tissue_type="brain" gene="mKIAA1526" 'gene="mKIAA1526" .2610 gene FEATURES COMMENT

AUTHORS TITLE JOURNAL

Gaps 36.4%; Score 610.2; DB 10; Length 3178; B8.8%; Pred. No. 4.9e-131; tive 0; Mismatches 83; Indels 0; Conservative Similarity 660; Query Match Local Best Loca Matches

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ROD 15-MAR-2003

linear

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305 GCAICTCCCCCACCCTCGGGCCTGCCCCAGCCCCACGGTGGTGCCCCTGAGGCAGCAGGAGG 364

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AY227205
Rattus norvegicus CASK-interacting protein CIP98 (Cip98) mRNA, complete cds.
AY227205
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12 (bases 1 to 2763)

Yap,C.C., Liang,F., Yamazaki,Y., Muto,Y., Kishida,H., Hayashida,T.,

Hashikawa,T. and Yano,R.

Blashikawa,T. and Yano,R.

Direct Submitted (29-JAN-2003) Brain Science Institute (BSI), RIKEN, 2-1

Hirosawa, Wako, Saitama 331-0198, Japan

Location/Qualifiers
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                            TGCGGCGTGCCAAGGCCCACGAGGGCTTGGGGCTTCAGCATCCGTGGGGGGCTCGGAGCACG
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Similarity 87.8%; Score 585; DB 10; Length 2
Similarity 87.8%; Pred. No. 3.4e-125;
52; Conservative 0; Mismatches 85; Indels
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2902)

Direct Submission

Submitted (15-AUG-1999) MIPS, Am Klopferspitz 18a, D-82152

Martinaried, GERMANY

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing

Consortium of the German Genome Project.

This clone (DKFZp434NO14) is available at the RZPD in Berlin.

Please contact the RZPD: Reseourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Futther

information about the clone and the sequencing project is available at http://www.mips.blochem.mpg.de/proj/CDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSM800885 2902 bp mRNA linear PRI 18-FEB-2000 Home sapiens mRNA; cDNA DKFZp434N014 (from clone DKFZp434N014);
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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                       1145 gcarcaccaacrcagcaggerr 1167
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Length 2902;

Score 554.8; DB 9; Pred. No. 3.5e-118;

33.1%; 99.6%;

Query Match Best Local Similarity

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Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Masubo,Y.
Full-length cDNAs
Full-length cDNAs
Patent: BP 1293569-A 782 19-MAR-2003;
Helix Research Institute (JP); Research Association for
Biotechnology (JP)
Biotechnology (JP)
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25.1%; Score 420.2; DB 6;
Best Local Similarity 95.0%; Pred. No. 5.6e-87;
Matches 434; Conservative 0; Mismatches 23;
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         AC131430
AC131430.3 GI:25007366
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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3 Isogal, T., Otsuki, T. and Sugiyama, T.
3 Isogal, T., Otsuki, T. and Sugiyama, T.
3 Isogal, T., Otsuki, T. and Sugiyama, T.
4 Isogal, T., Otsuki, T. and Sugiyama, T.
5 Isogal, T., Otsuki, T. and Sugiyama, Kisarazu, Chiba 292-0812, Japan Genomics Laboratory; 1532-3 yana, Kisarazu, Chiba 292-0812, Japan (E-mali spenomicsahiri oro.jp, Teli 81-438-52-3976, Fax:81-438-52-3986)
NEDO human CDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Blotechnology (RAB); CDNA ilbrary construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Blotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and
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1718 bp mRNA linear PRI 01-AUG-2002
Homo sapiens cDNA FLJ31628 fis, clone NT2RI2003344, weakly similar
to PRESYNAPTIC PROTEIN SAP97.
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Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
Kadaira, H., Furuya, T., Takahashi, M., Xikkawa, E., Omura, Y.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishi, S.,
Yamamoto, J., Isono, Y., Kawai-Ho, Y., Sato, K., Nishikawa, T.,
Kimura, K., Yamashita, H., Marsuo, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fuji, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
NEDO human cDNA sequencing project
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AKO56190.1 GI.16551526
Homo sapiens (human)
Homo sapiens
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CE Itoases 1 to 237250,

Ruzny, D. Marie, W. Matsheoke, S. Amin, A. Anguiano, D.,

Anyalebechi, V. Anyagi, A. Angodeji, W. Baca, B. Baden, H.

Baldin, D. Bandaranake, D. Barberak, S. Baden, H.

Baldin, D. Bandaranake, D. Barberak, S. Baden, H.

Baldin, D. Bandaranake, D. Barberak, S. Baca, Brown, M.

Baldin, D. Bandaranake, D. Garber, W. Blyth, P. Brown, M.

Bardana, V. Career, C. Cavaci, Casasa, H. Center, A. Chu, J.

Cardenas, V. Career, C. Bardy, Carcil, L. De Anda, C. Dedarich, D.

Davila, M. Dagar Rocha, S. Dunn, A. Durbin, K. Duval, B. Eaves, K.

Barnander, S. Filly, M. Flaggi, N. Probes, L. Boster, M.

Pernander, S. Filly, M. Flaggi, N. Probes, L. Boster, M.

Pernander, S. Filly, M. Flaggi, N. Probes, L. Garner, M.

Gabregocrgis, B. Geer, K. Gill, R. Gardy, M. Garra, M.,

Gabregocrgis, B. Geer, K. Gill, R. Gardy, M. Garra, M.,

Gabregocrgis, B. Geer, K. Gill, R. Gardy, M. Garra, M.,

Gabregocrgis, R. Haldy, M. Fland, S. Handerson, N. Harnander, J. Ackson, A.

Harnander, S. Kelly, S. Haldy, M. Fally, M. Kadly, S. Man, S. Maldy, M. Maldy, M. Maldy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Mandy, M. Man
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On Nov 15, 2002 this sequence version replaced gi:23664478 reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.ngsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Mithin each contig-scaffold, individual sequence contigs are ordered and oriented, and separated
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(Dases 1 to 237260)

Rat Genome Sequencing Consortium.

Birect Submission

Submitted (22-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

(bases 1 to 237260)

Rat Genome Sequencing Consortium.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                Center: Baylor College of Medicine
Center: Cadé: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: project name: GMYW
Center project name: GM30-133E19
Center clone name: CH230-133E19
Consensus quality: 227218 bases at least Q40
Consensus quality: 2229137 bases at least Q30
Consensus quality: 2293137 bases at least Q30
Consensus quality: 223933 bases at least Q30
Consensus quality: 223933 bases at least Q30
Consensus quality: 230333 bases at least Q30
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Consensus quality: 230333 bases at least Q30
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Consensus quality: 230338 bases at least Q30
Consensus quality: 230338 bases at least Q30
Consensus quality: 2000 bases; sum-of-contigs estimation
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole senome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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10.7%; Score 180; DB 2; Length 237260;
Best Local Similarity 70.0%; Pred. No. 6.5e-31;
Matches 291; Conservative 0; Mismatches 110; Indels 15; Gaps
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230853. .231688
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Score 180; DB 2;
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/mol_type="genomic DNA"
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/clone="CH230-164M17"
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213898. 215752
/note="wgs_contig"
32494. 333531
/note="wgs_contig"
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Disses I (Dases I to 333531)

Allen C. Allen, H. Alsbrooks S. Amin A. Arguiano, D. Alder, J. Algodeji, M. Bacas, E. Baden, H. Balancoks, J. Arguiano, D. Alder, J. Algodeji, M. Ayodeji, M. Ayodeji, M. Barnstead, M. Benahmed, F. Baldwin, D. Bandaranaike, D. Barnstead, M. Bernahmed, F. Baldwin, D. Baldwaio, K. Blar, J. Blankenburgk, Blyth, P. Brown, M. Barante, M. Bernahmed, F. Barden, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Davila, M. Davis, J. Casaz, J. Davila, M. Davis, J. Casaz, J. Davila, M. Davis, J. Casaz, J. Davila, M. Davis, J. Casaz, J. Davila, M. Davis, J. Casaz, J. Davila, M. Davis, J. Casaz, J. Davila, M. Davis, J. Casaz, J. Davila, M. Davis, J. Casaz, J. Davila, J. Casaz, J. Davila, J. Casaz, J. Davila, J. Casaz, J. Davila, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Casaz, J. Lau, J. Lau, J. Casaz, J. Casaz, J. Lau, J. Lau, J. Casaz, J. Casaz, J. Lau, J. Lau, J. Casaz, J. Casaz, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau, J. Lau,
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Satus norvegicus clone CH230-164M17, WORKING DRAFT SEQUENCE.
AC127863

AC127863.3 GI:25139795

HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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779 CAGGGCCATITCTGAAAGCCAGTGATAGCTGC--CTCCCATCCCTCCACCGCCCTGGCTC 836
                                                                                                                            837 ICCICICAGCCIGCAGICCCCACACCAGGCCCTCCATIGGCAGGACAIGACCIGGGCAC 896
                                                                                                                                                                                                                                                                                     219865 CTTCCCCTCCTCTCCTAGCCCCAGTGTCCTCACAGAAAGCTGAAAGTGCAGCACACA 219810
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AC127863
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Incarion/Qualifiers
                                                                                                                                                                                                                                                                          Worley,K.C.
Direct Submission
Submission
Submission
Submission
Submission
Modecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 333531)
Rat Genome Sequencing Consortium.
Direct Submission
Direct Submission

Worley, K.C.
Direct Submission
William Genome Sequencing Center, Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
Direct Submission
Unpublished
2 (bases 1 to 333531)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 333531;
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http://www.sanger.ac.uk/Projec from the RPCI-23 Mouse PAC Lib constructed by the group of Pi	VECTOR: pBACe3.6	Center code: UK-MRC Web site: http://mrcseq.har.ml Contact: mouseq@har.mrc.ac.uk	This sequence is the entire in right end of clone RP23-6H1 is Location/Oualifiers	1214370 organism="Mus muscu: mol type="lgenomic Di Ah Vref="! # avon 1000			1142911482,14299. 1517615229,15986. 2030420357,23140. 2829128344,29180.	31602. 31555,31880. 33068. 33175,35048. 38049. 38102,38249. 39742. 39768,41448. 44900. 45118,46780. 42000. 45118,46780. 42000. 45118,46780. 7product="bM340H1.1"	Em: B1597682 Em: BE683 Em: AW658049 Em: BE756 Em: BM545183 Em: AW446 /evidence=not experi	JOIN (<2.4%	31602. 31655,31880 33068. 33175,35048. 38049. 38175,35048. 38747. 38748.41448.	44900. 45118,46780. /gene="bM340H1.1" /note="match: protein for beta for
			FRATURES	source	misc feature	gene			i i	SCDS		
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291; Conservative 0; Mismatches 110; Indels 15; Gaps 3; 539 AGGTTGGGGACCAGATTCTAGAAGTGAATGGGGGGAGCTTTCTCAACATCCTACAGGACGA599		81 AGGCAGTGAAGCTGCTCAAGTCATCCCGGCACCTCATCCTGACCGTGAAGGACGTCGGGA	659 GGCTGCCCATGCCGCACCTGTGCACGAGACCAAGTGGATCGCCAGTTCCCGGATCA 718	719 GGGAGACCAIGGCGAACTCGGCAGGGTCTGGCCACTCTGCTCGCTCCAGATCTCCAGGACC 778	779 CAGGGCCATTICTGAAAGCCAGTGATAGCTGCCTCCCATCCTTCCACCGCCTGGCTC 836	837 TCCTCTCAGCCTGCAGTCCCCACACGAGGCCTCCATTGGCAGGCA	897 ATCCTTCTCTTGGCCTCAGTTTCCCCATGGAAAGCTGAAATACACCATCCA 952 	AL683828 AL683828 ION Mouse DNA sequence from clone RF21-340H1 on chromosome 4 Contrains to a fight of the gene for a novel collagen triple helix repeat and fibrillar collagen C-terminal domain containing protein, the Orml, Orm2 and Orm3 genes for orosomucoid 1, 2 and 3, an orosomucoid pseudogene, the gene for a novel protein similar to human AT-hook protein AKNA, gene 4933437N03R1k, gene 1110035G0731k (C430046P22R1k) and two CpG islands, complete sequence.	AL683428 AL683428. GI:21212361 HTG; 1110035G07Rik; 4933437N03Rik; C430046P22Rik; collagen; CpG island; Orml; Orm2; Orm3; orosmucoid. Mus musculus (house mouse)	M Mus musculus Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 214370)		hundrary@asnger.ac.uk Clone requests: clonerequestwesnaper.ac.uk On May 25, 2002 this sequence version replaced gi:20218659. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only asmall overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw.; SWISSPROT; Tr., TREMBL; WORMPEP; Information on the WORMPEP
Matches Oy	371 dd		Oy Db 178	Oy Db 17	Oy Db 17	Oy Db 17	Oy Db 17	RESULT 11 AL683828/c LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE	ORGANISM REFERENCE	AUTHORS TITLE JOURNAL	COMMENT

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from the Merci-12 Mouse brC Library Celegans/wormpep RE23-340H1 is from the Merci-22 Mouse brC Library Celegans/wormpep RE23-340H1 is constructed by the group of piecer de Jong.

PORTOR: PBAC63.

PORTOR: PBAC63.

Center: UK Medical Research Council
Center: Condec UK.WC

When the Merci-22 Mouse BrC Library Celegans Chicago Chorac.htm

Center: Condec UK.WC

When the Merci-22 Mouse Center
Center Code UK.WC

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VQGLRGEPGQQQQPGHPGPRGRPGPKGSKGEEGPKGKPGKAGPSGRRGTQGLQGLPGP RGVVGRQGPEGTAGSDGI PGRDGRPGYQGDQGNDGDPGPVGPAGRRGNPGVAGI PGAQ GPPGFKGESGLPGQLGPPGKRGTEGGTGLPGNQGEPGSKGQPGDSGEMGFPGVAGI.PG

PKGPPGDIGFKGIQGPRGPPGLMGKEGIIGPPGMLGBSGLPGPKGBRGSRGDLGLQGP
RGPPGPRGPRGPPGPWHPIOPQQDDLGAAFQTWMDAQGAVTSEGYSPDQLALDQGG
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PGRSSARQAVRFRANNCQVFBAGGQFRPEVSMDGCKVHDGRWHQTLFTFRTQDPQQLP
IVSVDNLPPVSSGKQYRLEVGPACFL" complement (471. 508)
/note="CYRA11 NM repeat: matches 401. .438 of consensus"
complement (509. 719)
/note="URN1A repeat: matches 1. .226 of consensus"
complement (720. 767)
/note="CYRA11_NM repeat: matches 148. .401 of consensus" 7.3265. 5278
/note="2.0 copies 7 mer GGGGTG 28% conserved"
complement(5544. 5635)
/note="MIR repeat: matches 46. .138 of consensus"
/note="MIR repeat: matches 7857. .7978 of consensus"
/note="MIMD3 repeat: matches 7857. .7978 of consensus" 4328. .4338 //note="11.0 copies 1 mer A 22% conserved" 4351. .4376 /note="3.0 copies 2 mer GT 43% conserved" 4410. .4437 /note="3.3 copies 12 mer TGTGCATCTCTG 38% conserved" 171. .2182

// note="2.0 copies 6 mer TTCCTG 24% conserved"
complement (26.0. .249)
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// note="14" // 4533. .4599 /note="23.5 copies 2 mer TG 24% conserved" 4555. .4602 /note="6.0 copies 8 mer TGTGTGTC 32% conserved" 6529. .6540 670ce="1.4 copies 5 mer AGCCC 24% conserved" 670ce="2.0 copies 7 mer CCTCTCC 28% conserved" 652. .6505 5053. .5063 //Anche="2.2 copies 5 mer TGGGC 22% conserved" 2225. .5236 //note="2.0 copies 6 mer GAGCTI 24% conserved" 1787. 4816 /note="5.0 copies 6 mer ACACAT 37% conserved" .5 copies 4 mer AGAA 148% conserved" 100. .6120 hote=14.2 copies 5 mer CCCTG 24% conserved" 428. .65.2 copies 4 mer AGAA 148% conserved" hote="18.5 copies 4 mer AGAA 148% conserved" _note="match: GSS: Em:AZ383735" 1052. .4061 .note="2.5 copies 4 mer ACCC 20% conserved" 1503. .4533 'note="15.5 copies 2 mer TG 62% conserved" 0 copies 2 mer CA 33% conserved" mer AGG 36% copies 3 3851. .4385 /gene="bM340H1.1" 7612. .7629 /note="6.0 co 784. .4813 note="15.0 repeat_region misc_feature

copies 4 mer GGAG 20% conserved"

7625. .7634 /note="2.5 co 7747. .7764

repeat_region

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186488 AGGCTCTCAAAGGCTCCAAGAAGCTGGTGCTGTGTATACTCAGCTGGGCGTATCCCAG 186429
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Mus musculus chromosome 4 clone BAC279, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313
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Sciurognathi; Muridae; Murinae; Mus
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Submitted (17-7M-2001) Genome Analysis, Institute of Molecular

Submitted (17-7M-2001) Genome Analysis, Institute of Molecular

Biotechnology, Beutenberstr. 11, Jena 07745, Germany

* NOTE: This is a "working draft" sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186308 GGAGTACCCTCCACCTCCTGCAGAGTGAGAAAAAAGGTGAGATTGACACT 186254
            7797. 7807

/ note="11.0 copies 1 mer G 22% conserved"

complement(8155. 8227)

/ note="12.0 copies 1 mer G 22% conserved"

/ note="12.0 copies 10 mer CCACATCTGA 40% conserved"

/ say. 8408

/ copies 10 mer CCACATCTGA 40% conserved"

8579. 8658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 GGGGCTACGTCACCAACCACATCTACACCTGGGTGGACCCGGCAGGCCGCCAGCATCTCCC
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                                                                                                                                                                                                                                                                                                                                                        Query Match
10.3%; Score 172.6; DB 10; Length 214370;
Best Local Similarity 83.4%; Pred. No. 3.3e-29;
Matches 196; Conservative 0; Mismatches 39; Indels 0; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAGCACCCTGCACCTGCAAGGAGGGGGATGAGAAAAAGGTGAACCTGGTGCT
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/note="B4A repeat: matches 5. .287 of consensus"
9083. .9093
/note="2.2 copies 5 mer TCCTG 22% conserved"
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'note="3.0 copies 6 mer ACAAGG 27%
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Mus musculus (house mouse)
Mus musculus
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MACOLOGOS 2 GI:6996798

ACOLOGOS PARENTS:
Drosophila melanogaster (fruit fly)
Drosophila melanogaster (fruit fly)
Drosophila melanogaster (fruit fly)
Drosophila melanogaster (fruit fly)
Brancotti Messel to coophila melanogaster (fruit fly)
Meorters Endopteryqueta; Diptera; Brachyceta; Muscomorpha;
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                                         14493 GACGAGGCGGTGAGTTGAAGTACCACAAACGCATGTCGCTGGTGATACGTGACGTG 14434
                                                                                                                                                                                                                                                              ACO10699 63934 bp DNA linear HTG 18-FEB-2000 Drosophila melanogaster clone RPC198-25L10, *** SEQUENCING IN PROGRESS ***, 39 unordered pieces.
GACGAGGCTGTTAAGTCATCTCGGCACCTCATCCTGACAGTGAAGGACGTC 654
                                                                                                                                        * NOTE: This is a 'working draft' sequence. It currently * consists of 39 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                   655 GGGAGGCTGCCCATGCCCACTGTGGACGACCAAGTGGATCGCC
       595
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AUTHORS
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AC010699
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Direct Submission

Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,

Rockville, MD, USA

This sequence was identified as CDM:10211077 by the submitter.

For further information on this sequence e-mail to fly@celera.com.

* Nors: This is a "working draft" sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers

1. 16325

rce /organism="Drosophila melanogaster"

//db_xref="texon:7227"
                                                                                                                                                                                                                                                                                                                                                                                 191195 AGGITGGAGACCAGAITCIGGAGGTGAATGGGCGGAGCTITCTCAACAICCTGCAFGATG 191136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC015144 16-NOV-1999 DNA linear HTG 16-NOV-1999 Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***. AC015144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        475 TACGGCCTTGGCATTTACATCACTGGCGTGGACCCAGGCTCTGAAGCAGAAGGCAGCGGG 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCAAGGTTGGGGACCAGATTCTAGAAGTGAATGGGCGGAGCTTTCTCAACATCCTACAC 594
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                                                                                                                                                                                                                                                                                                                                                          AGGCTGTCAGGCTGCTTAAGTCATCTCGGCACCTCATCTGACAGTGAAGGACGTCGGGA 658
                                                                                                                                                                                                                                                         539 AGGITGGGGACCAGATICTAGAAGTGAATGGGCGGAGCTTTCTCAACATCCTACACGACG
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HTG; HTGS PHASE2.

Drosophila melanogaster (fruit fly)

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Phydroidea; Drosophilidae; Drosophila.

Adams, M. and Venter, J.C.
                                                                                                                                                                                                            0; Gaps
                                                                                                                                                        10.2%; Score 171.8; DB 2; Length 219809; llarity 87.4%; Pred. No. 5.1e-29; Conservative 0; Mismatches 27; Indels 0; C
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6.5%; Score 108.6; DB 2; Length 16
Best Local Similarity 60.8%; Pred. No. 1.6e-14;
Matches 177; Conservative 0; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191015 GGGAAGGGTCGCCAACTCAGGGTCTGGGTCTC 190981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            719 GGGAGACCATGGCGAACTCGGCAGGGTCTGGCCAC 753
               /mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="4"
/clone="BAC279"
                                                                                                                                                                                       Similarity
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/organism="Drosophila mel
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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-MODBL=frame+ p2n.model -DEV=xlp
-MODBL=frame+ p2n.model -DEV=xlp
-MODBL=frame+ p2n.model -DEV=xlp
-De-/Cap2_1/USPTO spool_p/US10078090/runat_20042004 132810 16588/app_query.fasta_1.455
-De-/Cap2_1/USPTO spool_p/US10078090/runat_20042004 132810 16588/app_query.fasta_1.455
-DEV_ALIGN=200 -THE_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                             April 21, 2004, 21:36:07; Search time 3091 Seconds (without alignments) 3645.807 Million cell updates/sec
                                                                                                                                                                                                                         US-10-078-090-151
1326
1 LRRAKAHEGLGFSIRGGSEH......TMANSAGSGHSARSNLQTPG 260
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                        OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                         3470272 segs, 21671516995 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                      0.5
0.5
0.5
                                                                                                                                                                                                                                                                                                             BLOSUM62
Xgapop 10.0, Ygapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, belext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                  Run on:
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/codon_start=2 /product="KIAA1526 protein" /protein_id="BAA96050.1" /db_xref="GI:/959319" /translation="SPRPPRIQPLYPCSPNPGSSRRLRAPGDPAVAPVPARTAAPPTP GVGÍTVSLVEPGSLAEKEGLRVGDQILRVNDKSLARVTHAEAVKALKGSKKLVLSVYS AGRIPGGYVTNHÍYTWVDPQGRSISPPSGLPQPHGGALRQQEGDRRSTLHLLQGGDBK KVNLVLGDGRSLGLTIRGGAEYGLGIYITGVDÞGSEAEGSGLKVGDQILEVNGRSFLN Submitted (104-APR-2000) Osamu Ohara, Kazusa DNA Research Institute, Submitted (104-APR-2000) Osamu Ohara, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.xazusa.or.jp/huge, Tel:81-438-52-3913, Fax:81-438-52-3914) ralrarpolgyemmaploglsyssstgslgsragagggggaglrllsanvrolhgal tallseaerropthclnayharrnypolvrtlrylldspykrrllpmlrly1prsdol lfdoytaeglylpattpyropawggpdsagpgevrlyslrrakahbglgfstrggseh PRI 22-FEB-2001 Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites) /gene="KIAA1526" hote="Etart codon is not identified. fj04743 cDNA clone for KIAA1526 has a 1196-bp insertion after the position 1335 of the sequence of KIAA1526." Nagase, T., Kikuno, R., Ishikawa, K., Hirosawa, M. and Ohara, O. Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro
DNA Res. 7 (2), 143-150 (2000) AB040959 3566 bp mRNA linear I formo sapiens mRNA for KIAA1526 protein, partial cds. AB040959.1 GI:7959318 /organism="Homo sapiens"
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/clone="fj04743" Ohara, O., Nagase, T. and Kikuno, R. Direct Submission Homo sapiens (human) (bases 1 to 3566) Homo sapiens DNA Res. 10819331 AB040959 LOCUS DEFINITION ACCESSION VERSION KEYWORDS Bource ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL gene CDS FEATURES

LIHDEARALLKESKHILITUVKDVGRLIHARTTVDETKRIASSRIKETVANSAGELGDI TYEGINKPEPEYKGPAGSQVTLASSLGOVRVLLEBOQAHLLINDEHATNYLDETKRG SVSVBALLWALLKELTHTAKRSILLSEVRGTISPQDAHLLINDEHATSIESKRKAQPPO SVSTSQCALSSKRLPREPELSEVRGTISPQDANTLDLEBTGEAVGONINALPDVSVDD NSTSQCALSSKRLPREPELAGNDLPHOGPRALGRBLLQPRESMPSGGGTVFBAPQN RSTSQCALSSKRLPREPESSYADLESSTANSANPSSKRPLDAHLALVNQHPIGPFRVD RSPPAGTTAPTGGTSAQLLPSPSGHPDQTGTNQHFVWVFVHRPDSSPDVNEVRALP SCHTAGTISCALSDSGVTLSEDSGVDAGSBARARSFGRRQVGVSTKRSRSKELPRNERPT DGANKPPGLLBFTSTLVRVKKKSAATIGIAIEGGANTRQPLPRIVTIRPTGGGL KVGHVILEVNGITLRGKEHREAARIIABAFKTKDRDYIDFLVTFFNVML"

ORIGIN

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1.43e-72 1261.50 96.17% 95.79% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB:

US-10-078-090-151 (1-260) x AB040959 (1-3566)

1 LeuargargalalysalaHisGluGlyLeuGlyPheSerIleArgGlyGlyGerGluHis 20	21 GlyvalGlylleTyrValSerLeuValGluProGlySerLeuAlaGluLysGluGlyLeu 40	41 ArgvaldlyAspGlnIleLeuArgValAsnAspLysSerLeuAlaArgValThrHisAla 60	61 GlualaValLysalaLeuLysGlySerLysLysLeuValLeuSerValTyrSerAlaGly 80	81 ArgileproglyglytyrvalthrashHisiletyrThrTtpValaspProglnGlyarg 100	101 SerIleSerProProSerGlyLeuProGlnProHisGlyGlyAlaLeuArgGlnGlnGln 120	121 GlyAspArgArgSerThrLeuHisLeuLeuGlnGlyGlyAspGluLysLysValAsnLeu 140 	141 ValLeuGlyAspGlyArgSerLeuGlyLeuThrIleArgGlyGlyAlaGluTyrGlyLeu 160 	161 GlyllefyrllefhrGlyValAspProGlySerGluAlaGluGlySerGlyLeuLysVal 180	181 GlyaspGlnIleLeuGluValAsnGlyargSerPheLeuAsnIleLeuHisAspGluAla 200 	201 ValargLeuLeuLysSerSerArgHisLeuIleLeuThrValLysAspValGlyArgLeu 220 	221 ProHisAlaArgThrThrValAspGluThrLysTrpIleAlaSerSerArgIleArgGlu 240	241 ThrMetalaasnSeralaGlySerGlyHisSeralaargSerasnLeuGlnThrPro 259	260 Gly 260 1 1376 GGA 1378	AK12253 AK12253 AK12253 AK12253 AK12253 AK12253 AK12253 AK12253 AK12252 AK12252 AK1252 AK1
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RLVSLRRAAHBGIGFS: RRGGSEHGVG1YVELNERGSLRVGDQILKVNDKSL
RLVSLRRAXAHBGIGFS: RRGGSEHGVG1YVELNERGSLRVGDQILKVNDKSL
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GSTLLSGREXTHANTVTLAQYRGGTISVERAMAALFILITYVNDVGRLPHARTTVD
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LDLEGTGETTGGSTNALPDVSVUDVKSPSEDLPGIKPPPPPPLAGGGHGTTVSRANT
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RRFLDTHLALVNQHPRIGPPRVQSPPHLKSPPATPGAGACLPPPSPSEBHPDAVGANQ
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RQPLPRIVTIORGGSAHNCGGLKVGHVILEVNGGTLRRGFAARIIAEAFKTKRRD
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cDNA clones randomly sampled from size-fractionated libraries
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Matches:
Conservative:
Mismatches:
Indels:
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/gene="mKIAA1526"
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1196.50
92.72*
90.80*
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Best Local Similarity:
Query Match:
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Pred. No.:
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REFERENCE
AUTHORS
TITLE
JOURNAL
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AY227205
Rattus norvegicus CASK-interacting protein CIP98 (Cip98) mRNA, complete cds.
AY227205
AY27205.1 GI:29373052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 2763)

Yap,C.C. Liang,F., Yamazaki,Y., Muto,Y., Kishida,H., Hayashida,T.,
Hashikawa,T. and Yano,R.

Direct Submission
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                                                                                                             120
                                                                                                                                                                    140
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                         558
                                                                                                                                                                                                                                                                                                                                         181 GlyAspGlnIleLeuGluValAsnGlyArgSerPheLeuAsnIleLeuHisAspGluAla
                                                                                                                                                                                                                                                                                                                                                            859 GGAGACCAGATTCTGGAGGTGAATGGGCGGAGCTTTCTCAACATCCTGCATGATGAGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                   241 ThrMetAlaAsnSerAlaGly---SerGlyHisSerAlaArgSerAsnLeuGlnThrPro
                                                                                                                              121 GlyAspArgArgSerThrLeuHisLeuLeuGlnGlyGlyAspGluLysLysValAsnLeu
                                                                                                                                                                                        ValLeuGlyAspGlyArgSerLeuGlyLeuThrileArgGlyGlyAlaGluTyrGlyLeu
                                                                                                                                                                                                                                                   139 GIGTIGGGGGGCGCGGTCCTIGGGCCTCACGAICCGAGGTGGAGCAGAGTACGGCTT
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                                                                             CGTATCCCAGGGGCTATGTGACCAACCACTTTATATACTGGGTGGACCCAGGGTCGA
                                                                                                             SerlleSerProProSerGlyLeuProGlnProHisGlyGlyAlaLeuArgGlnGlnGlu
                ArgileProGlyGlyTyrValThrAsnHisIleTyrThrTrpValAspProGlnGlyArg
GlualavallysalaLeuLysGlySerLysLysLeuValLeuSerValTyrSerAlaGly
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Rattus norvegicus
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QALTALLSEPEREQFINCLINYHARRNVFDLVRTLRYLLDSBVKRRLLEMIELVIFSS
QALTALLSEPEREGFINCHCLINYHARRNVFDLVRTLRYLLDSBVKRRLLEMIELVIFSS
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Matches:
Conservative:
Mismatches:
Indels: organism="Rattus norvegicus" mol type="mRNA" strain="WST" protein_id="AAO72534.1" db_xref="GI:29373053" US-10-078-090-151 (1-260) x AY227205 (1-2763) Gaps: /db_xref="taxon:10116" 1. . . 2763 /gene="Cip98" 1. .2763 /gene="Cip98" /note="98 kDa" 5.74e-66 1157.50 90.80% 88.89% Percent Similarity: Best Local Similarity: Query Match: DB: Scores: 19 141 source .. oN . Alignment gene CDS ORIGIN

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HSM800885 2902 bp mRNA linear PRI 18-FEB-2000
Homo sapiens mRNA; cDNA DKFZp434N014 (from clone DKFZp434N014);
partial cds.
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              .024 GTGAAGGTGCTCAAGTCATCCCGGCACCTCATCCTGACCGTGAAGGACGTCGGAGGAGGTG
                                           221 ProHisAlaArgThrThrValAspGluThrLysTrp1leAlaSerSerArg1leArgGlu
                                                                241 ThrMetAlaAsnSerAlaGly---SerGlyHisSerAlaArgSerAsnLeuGlnThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="DKFZp434N014"
/note="similarity to NY-CO-38 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="hypothetical protein"
protein id="CAB53685.1"
db_xref="G1:S817167"
db_xref="G03:Q9UF23"
db_xref="GPTREMBL:Q9UF23"
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| organism="Homo sapiens"
| mol_type="mRNA"
| db xref="texon:9606"
| clone="DKFZp434N014"
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964 GGGACCAGATICTGGAGGTGAACGGGCGAACCTTCTCAGCATCCTGCATGACGAGGCA

904 GGCATTTACATCACTGGTGTGGACCCGGGCTCTGAAGCCGAAAGCAGCGGCCTCAAGGTT GlyAspGlnIleLeuGluValAsnGlyArgSerPheLeuAsnIleLeuHisAspGluAla

GlyIleTyrIleThrGlyValAspProGlySerGluAlaGluGlySerGlyLeuLysVal

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GTGCTGGGGGACGGCCGGTCCTTGGGCCTCACAATCCGAGGTGGAGCCGAGTACGGCCTT

/translation="KLLGGSRGPRLLPPECRSVACVQALKGSKKLVLSVYSAGRIPGGY
VTNHIYTWVDPGGRSISPPSGLPQPHGGALRQDEGDRSTLHLLGGGDEKKYNLVLGD
GRSLGGTIRGGABSTGLGIYITGVDFGSEBEGGSLKVGDQILEVWGRSFLNILLDBAVR
LLKSSRHLILTVWDVGRLPHATTVDFTKMIASSRIBETWARNSAGFLGDLTTFGINKP
GFYKGPAGSQYTLSSLGNGTRYLLEGARHLLNBGERATWAYYLDEYRGGSVOEALV
MALFKILLNTHAKFSLLSSUGGTISPQDLERFDHLVLRRETESTRAMYDDFYRGGSVOEALV
MALFKLLNTHAKFSLLSSVGGTISPQDLEFDGAVQGNINALDEDVSVDDVRGTSGGL
SFFEDPRPPLAGGNDLPLGGPRKLGREDLQPPSSMPSGSGTVSAPPRGGSTGGL
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PTPGTSSAQDLPSSPPIAGSPRANTBOHRANDSPDVNBVRALPQTFTASP
SQLSSDGGTLLSPSSDGVDAGERASAFGRGRGSVSTKSRSSKELPRNBRPTDGANKPPG
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/ Gene="DKFZP434N014"
/ Gene="DKFZP434N014"

RESULT 5

polyA_signal polyA_site

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1.27e-52 951.50 89.95% 87.21% 71.76% Alignment Scores:
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ò	43 GlyAs	GlyAspGlnIleLeuArgValAsnAspLysSerLeuAlaArgValThrHisAlaGluAla 62
qq	20 GGCCC	GGCCCACGACTACTTCCTCCTGAGTGCCGTTCAGTG3CCTGT 61
ò	63 Vally	VallysAlaLeuLysGlySerLysLysLeuValLeuSerValTyrSerAlaGlyArgIle 82
qa	62 GTCCA	GGCTCTGAAGGGCTCCAAGAAGCTGGTGCTGTTGTTGTTCTCAGCAGGGCGCATC 121
ò	83 ProGl	ProGlyGlyTyrValThrAsnHisIleTyrThrTrpValAspProGlnGlyArgSerIle 102
qq	122 CCTGG	GGGCTACGTCACCAACCACATCTACACCTGGGTGGACCCGCAGGGCCGCAGCATC 181
ò	103 SerPr	SerProProSerGlyLeuProGlnProHisGlyGlyAlaLeuArgGlnGlnGluGlyAsp 122
QQ	182 TCCCC	ACCTTCGGGCCTGCCCCAGGCCCCACGGTGCCCTGAGGCAGCAGGAGGAGGTGAC 241
ò	123 ArgAr	ArgArgSerThrLeuHisLeuLeuGlnGlyGlyAspGluLysLysValAsnLeuValLeu 142
Db	242 CGGAG	GAGCACCCTGCACCTCCTGCAAGGAGGGGATGAGAAAAAGGTGAACCTGGTGCTG 301
à	143 GlyAs	GlyAspGlyArgSerLeuGlyLeuThrlleArgGlyGlyAlaGluTyrGlyLeuGlyIle 162
Dp	302 GGGGA	CGGCCGGTCCCTGGGCCTCACGATCCGTGGGGGAGCTGAGTACGGCCTTGGCATT 361
ò	163 Tyril	TyrileThrGlyValAspProGlySerGluAlaGluGlySerGlyLeuLysValGlyAsp 182
Db	362 TACAT	CACTGGCGTGGACCCCAGGCTCTGAAGCAGAGGCGGGGCTCAAGGTTGGGAC 421
ò	183 GlnIl	GInIleLeuGluValAsnGlyArgSerPheLeuAsnIleLeuHisAspGluAlaValArg 202
qq	422 CAGAT	TCTAGAAGTGAATGGGCGGAGCTTTCTCAACATCCTACACGACGAGGCTGTCAGG 481
ò	203 LeuLe	LeuLeuLysSerSerArgHisLeuIleLeuThrValLysAspValGlyArgLeuProHis 222
qq	482 CTGCT	TAAGTCATCTCGGCACCTCATCCTGACAGTGAAGGACGTCGGGAGGCTGCCCCAT 541
ò	223 AlaAr	AlaargThrThrValAspGluThrLygTrpIleAlaSerSerArgIleArgGluThrMet 242
qq	542 GCCCG	CACCACTGTGGACGAGGCCAAGTGGATCGCCAGTTCCCGGATCAGGGAGACCATG 601
ŏ	243 AlaAs	AlaAsnSerAlaGlySerGlyHisSerAlaArgSerAsnLeuGlnThrProGly 260
, QQ	602 GCGAA	CTCGGGAGGGTTTCTTGGCGATCTCACAACAAGGAATAAACAAGGA 658

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Manmalia, Eutheria, Primates, Catarrhini; Hominidae, Homo.

To (bases 1 to 1865)

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Generation and initial analysis of more than 15,000 full-length
human and mouse const. Disc., 92,882,71
Parson, Natl., Acad., Sci. U.S.A., 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC029054 Homo sapiens hypothetical protein FLU33209, mRNA (cDNA clone MGC34150 IMAGE:5179973), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                      121 GlyaspargArgSerThrLeuHisLeuLeuGlnGlyGlyAspGluLysLysValAsnLeu 140
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Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                        101 SerileSerProProSerGlyLeuProGlnProHisGlyGlyAlaLeuArgGlnGlnGlu
                                                       41 ArgValGlyAspGlnIleLeuArgValAsnAspLysSerLeuAlaArgValThrHisAla
                                                                                                                                  1256 GAGGCCGTCAAGGCTCTGAAGGGCTCCAAGAAGCTGGTGTGTTGTTGTACTCAGCAGGG
                                                                                                                                                                                                                                                                                         81 ArgileProGlyGlyTyrValThrAsnHisIleTyrThrTrpValAspProGlnGlyArg
                                                                                                                                                                                                                                                                                                                               GlyvalGly11eTyrValSerLeuValGluProGlySerLeuAlaGluLysGluGlyLeu
                                                                                                                                                                                                   61 GluhlaValLysAlaLeuLysGlySerLysLysLeuValLeuSerValTyrSerAlaGly
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Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
Kodaira,K., Katsuta,M., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,K., Nishikawa,T.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
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Nikuchi,H., Murakawa,A., Kawakami,B., Suzuki,Y., Sugano,S.,
NEDO human cDNA sequencing project
Unpublished
CE 2 (bases 1 to 1718)
RS Isogai,T., Otsuki,T. and Sugiyama,T.
Direct Submission
AL Submission
RS Submitted (24-OCT-2011) Takao Isogai, Helix Research Institute,
Genomics Laboratory, 1552-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3965)
RSCONGWY, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library of Sconstruction: Helix Research Institute of Pechnology and FRI, and Biotechnology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Full insert sequencing: RAB and
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precursor cells treated 2-weeks mitotic inhibitor after
5-weeks retinoic acid (RA) induction.-majorly NT2 neuron"
650 .1687
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Matches:
Conservative:
Mismatches:
to PRESYNAPTIC PROTEIN SAP97.
AK056190
AK056190.
Grosping, fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
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94.59%
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Best Local Similarity:
Query Match:
DB:
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source

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

Pred. No.:

Score:

ORIGIN

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673

553

733 113 133

COMMENT

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60 AlaGluAlaValLySAlaLeuLySGlySerLySLySLeuValLeuSerValTyrSerAla 79
                                                                                                                                                                                                                      100 ArgSerIle------SerProProSerGlyLeuProGlnProHisGly
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                                                                                                                                                                                    LeuargvalGlyAspGlnIleLeuArgvalAsnAspLysSerLeuAlaArgValThrHis
                                                                                                                                                                                                                                                                                                                                                                                               GlyargileproGlyGlyTyrValThrAsnHisIleTyrThrTrpValAspProGlnGly
734 ceececeregragragaeagaegecegricaacaccricceac-----
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                                                                                                                                                                                                                                                                                                                                                                      clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov.Series: IRAK Plate: 50 Row: a Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21914924.
                               Email: cgapbs.rdmail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC.
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .1805

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/tissue_type="Brain, Lung, Testis, adult, pooled whole"

/clone_lib="MIH MGC_115"

/lab_host="DH103"

/note="Vector: pCMV-SPORT6"
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76. .1711
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gene="FLJ23209"
                      Contact: MGC help desk
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                                                                                                                                 154 GlyGlyAlaGluTyrGlyLeuGlyIleTyrIleThrGlyValAspProGlySerGluAla 173
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826
                                                                                     856
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Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Outpublished
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----AlaSerSerArgIleArgGluThrMetAlaAsnSerAlaGlySerGlyHisSer
                                         134 AspGluLysLysValAsnLeuValLeuGlyAspGlyArgSerLeuGlyLeuThrileArg
                                                                                                                                                              |||||||
857 GGGGGCAAGGAGTTTGGCCTGGGCATCTATGTGTCCAAAGTGGACCATGGTGGGCTGGCC
                                                                                       827 GACGAC-----TOTAGCTGCCTGGGCTTCAACATCCGT
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956

896 173 213

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http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL138895 132292 bp DNA linear PRI 27-JUN-2001 Human DNA sequence from clone RP11-9M16 on chromosome 9, complete sequence.
                                                                                                                                                                                                                                                                                                                                       234 -----AlaSerSerArgIleArgGluThrMetAlaAsnSerAlaGlySerGlyHisSer 251
                                                                                                                                                                                                                                             174 GluGlySerGlyLeuLysValGlyAspGlnIleLeuGluValAsnGlyArgSerPheLeu 193
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1. (bases 1 to 132292)
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                                114 GlyAlaLeuArgGlnGlnGluGlyAspArgArgSerThrLeuHisLeuLeuGlnGlyGly
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867 GACGAC------TTCTGCCTGGGCTTCAACATCCGT
                                                                                                                                                                             154 GlyGlyAlaGluTyrGlyLeuGlyIleTyrIleThrGlyValAspProGlySerGluAla
                                                                                                                                                                                              -----ACCAGGTCAGAAGATGGTGTCCGGCGC---ATCGTCCACACTATACACAACCTCC
                                                                                                  134 AspGluLysLysValAsnLeuValLeuGlyAspGlyArgSerLeuGlyLeuThrIleArg
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774 CGGCGCCTGGTAGTGGAAAGTGCGGTTCAACACCCCTCCGAC----
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VLKGQTHIMLTIKETGRYPAYKEMVSEYCWLDRLSNGVLQQLSPASESSSSYSSCASS
SPYSSGSLPSDRWDICLGQEEPGSRGPGWGRADTAMQTEPBAGGVVETWCSYREYLIL
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GGSEHGLGIFVSKVEEGSSAERAGLCVGDKITEVNGLSLESTTMGSAVKVLTSSSRLH
MMVRRMGRVPGIKFSKEKTTMVDVVNRRLVVEKCGSTPSDTSSEDGVRRIVHLYTTSD
                              Direct Submission.
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HisGlyValGlyIleTyrValSerLeuValGluProGlySerLeuAlaGluLysGluGly
Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,
Shibahara, T., Tanaka, T. and Nakamura, Y.
Direct Submission
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107
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Conservative:
Mismatches:
Indels:
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    .2037
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438.00
55.13*
40.68*
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Group. Further information can be found at http://www.aanger.ac.uk/HGP/Chr9
RP11-9M16 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBAce3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-9M16 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-9M16 is at 132292 in this sequence. The true left end of clone RP11-40033 is at 124695 in this sequence. The true right end of clone RP11-8211 is at 2000 in this sequence.
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note="L1MC1 repeat: matches 5718. .5955 of consensus"
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004e="MTR repeat: matches 82. .144 of consensus"
note="LTR16A repeat: matches 200. .354 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160. .8271
note="LTR16C repeat: matches 255. .368 of consensus"
0037. .10131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271. .2435
note="MER63A repeat: matches 46. .206 of consensus"
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1151. .11327
note="MIX repeat: matches 18. .205 of consensus"
1579. .11883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        467. .2553
note="MIR repeat: matches 79. .165 of consensus"
887. .2713
note="L2 repeat: matches 2622. .2740 of consensus"
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note="AluSc repeat: matches 5. .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299. .5606 — note="AluSx repeat: matches 12. .312 of consensus' 686. .5787 mote="MIR repeat: matches 141. .262 of consensus" 714. .6799 note="MIR repeat: matches 20. .114 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        995. 7437
note="MLT1D repeat: matches 3. .503 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214. .3262
note="MIR repeat: matches 115. .166 of consensus"
193. .4262
note="MIR repeat: matches 60. .130 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99. .696
motes"Alusg repeat: matches 1. .298 of consensus"
186. .1273
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2598. .12717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MIR repeat: matches 49. .142 of consensus"
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note="MIR repeat: matches 14. .123 of consensus"
0604. .10711
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note="AluY repeat: matches 1. .32 of consensus"
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368. .5308
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15216. .15653
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/note="Liz repeat: matches 2372. .2688 of consensus"
16113. .16847
/note="Liz repeat: matches 1940. .2707 of consensus"
16875. .16922
/note="MIR repeat: matches 1940. .2707 of consensus"
16875. .16922
/note="MIR repeat: matches 125. .230 of consensus"
17482. .17573
/note="MIR repeat: matches 23. .241 of consensus"
18972. .19080
/note="MIR repeat: matches 23. .241 of consensus"
18972. .20994
/note="MIR repeat: matches 23. .241 of consensus"
18121. .21521
/note="Liz repeat: matches 2045. .2158 of consensus"
21523. .21758
/note="MIR repeat: matches 1. .232 of consensus"
22863. .23788
/note="MIR repeat: matches 1. .232 of consensus"
22863. .237495
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22863. .23495 /note="Mark repeat: matches 1. .426 of consensus"
2315. .23495
/note="Mark repeat: matches 5. .192 of consensus"
24438. .24542
/note="Mar repeat: matches 28. .140 of consensus"
24933. .2526
/note="Mar repeat: matches 2099. .2709 of consensus"
25630. .25867
/note="Mark repeat: matches 16. .262 of consensus"
25639. .2633
/note="Mark repeat: matches 2363. .2674 of consensus"
26257. .26381 30658. 30770

John E. W. Consensus.

John E. W. Consensus.

John E. W. Consensus.

John E. W. Consensus.

John E. W. Consensus.

John E. W. Consensus.

John E. W. Consensus.

John E. W. Conserved.

John E. W. Conserved. Anote - Alusx repeat: matches 1. .298 of consensus" 29523. .2964
Anote - L2 repeat: matches 2593. .2734 of consensus" 2669. .29777
Anote - MIR repeat: matches 17. .140 of consensus" .2289 of consensus" Anote="Alusx repeat: matches 1. .303 of consensus" 35834. .35965 /note="MIR repeat: matches 2. .147 of consensus" note="MER5B repeat: matches 1. .173 of consensus" fnote="MIR repeat: matches 64. .147 of consensus" 77292. .27435 note="MIR repeat: matches 102. .254 of consensus" 9060. .29358 note="16 copies 2 mer to 84% conserved" 32426. .32485 fnote="MIR repeat: matches 96. .152 of consensus" 33041. .33127 3041. .33127 note="MIR repeat: matches 20. .115 of consensus" 3494. .33764 note="MIR repeat: matches 28. .153 of consensus" 6919. .27000 .207 of consensus" note="L2 repeat: matches 2167. 0460. .30627 note="MIR repeat: matches 8. 5436. .35738 repeat_region

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154016 ccreededchacerchchacchchrichachcheeredenadaccedadecheche 153957
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Rump, A., Varela, A., Mburu, P., Brown, S.D.M. and Rosenthal, A. Mouse chromosome 4 genomic sequence
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903: gap of unknown length
04 8454: contig of 7551 bp in length
55 8554: gap of unknown length
55 171627: contig of 163073 bp in length.
1.171627
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408.50
70.55%
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In May 25. 2002 this sequence version replaced gil20128659.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with conjy a small overlapping clone, as we submit sequences with conjy a small overlapping clone, as we submit sequences with conjy a small overlapping clone, as we submit sequences with conjy as small overlapping clone, as we submit sequences with conjy as a described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw;, SwiSSPROT; Tr;, TREMBL; Wp;, WORMPEP; Information on the WORMPEP database can be found at the their define the PRCI-23 Mouse PAC library constructed by the group of Fieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm
                                                                  AL681828

Mouse DNA sequence from clone RP23-340H1 on chromosome 4 Contains the 3' end of the gene for a novel collagen triple helix repeat and fibrillar collagen C-terminal domain containing protein, the Orml, orm2 and Orm3 genes for orosomucoid 1, 2 and 3, an orosomucoid pseudogene, the gene for a novel protein similar to human AT-hook protein AKNA, gene 4933437NO3Rik, gene 1110035607Rik (C430046P22Rik) and two CpG islands, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224. .48609 | Join (224. .268,511.") | Join (224. .268,511.") | Join (224. .268,511.") | Join (224. .268,511.") | Join (224. .268,511.") | Join (224. .268,511.") | Join (224. .268,514.") | Join (224. .268,514.") | Join (224. .268,514.") | Join (222,147) | Join (222,149) | Join (222,147) | Join (222,149) | Join (222,166,2. .16705,18803. .18856,2834) | Join (222,147) | Join (222,149) | Join (222,147) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (222,149) | Join (2222,149) | Join 
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 214370)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (17-OCT-2002) Wellcome Trust Sanger Institute, Hinxton,
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Location/Qualifiers

1. 214370
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AL683828 GI:21212361
HTG; IllO035G07Rik; 4933437N03Rik; C430046F22Rik; collagen; CpG
island; Orml; Orm2; Orm3; orosmucoid.
Mus musculus (house mouse)
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mol type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="4"
/clone="RR23-340H1"
/clone="RR23-340H1"
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/note="URRIA repeat: matches 1. .226 of consensus" complement(720. .767) /note="VRA11_MM repeat: matches 148. .401 of consensus"
33068 .33175,35048 .35155,37066 .37119,37537 .37599,38049 .38102,38249 .38284,38390 .38407,38737 .37899,39742 .3878,41448 .41513,42153 .42321,43416 .43525,7900 .45118,46780 .48609)
                                          /product="bM340H1.1 (novel collagen triple helix repeat and fibrillar collagen C-terminal domain containing protein)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: cDNAs: Em:AB058773 Em:AK003879 match: ESTS: Em:BB205277 Em:BB226911 Em:AV231828 Em:A449266 Em:AU120087 Em:AA296500 Em:AM652868 Em:Em:EDF602 Em:EDF68377 Em:AA296378 Em:AA29649 Em:EDF681878 Em:BB621398 Em:AA43633 Em:BM545183 Em:BM545183 Em:BM545183 Em:BM545183 Em:AM446832 Em:BF773650"
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RESULT 12
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complement(8155. .8227)

Thote="12 repeat: matches 3221. .3295 of consensus"
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/note="2.2 copies 5 mer TCCTG 22% conserved"
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vided by the submittor. s sequence will be replaced accession number will be preserved. 1 33351: contig of 33551 bp in length. Location/Qualifiers 1. 33551 / Arganism=Rattus norvegicus" //moi_type="genomic DNA" /db_xref="taxon:10116" /clone="cg1230-164M17" /note="wgs_contig" 213898. 215552 /note="wgs_contig" 332444. 335351 /note="wgs_contig"	NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have	ACCESSION VERSION KEYWORDS SOURCE ORGANISM
accession number will be preserved. 1 33351: contig of 33351 bp in length. Location/Qualifiers 133531 /organism="Rattus norvegicus" /moi type="genomic DNA" /db_xref="taxon:1016" /clone="CH230-164M17" 1125752 /note="wgs_contig" 3324433551 /note="wgs_contig" /note="wgs_contig"	provided by the submittor. This sequence will be replaced by the finished sequence as soon as it is available and	AUTHORS TITLE
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Nus musculus chromosome 4 clone BAC279, *** SEQUENCING IN PROGRESS
***, 3 unordered pieces.

NAF336379 1 GI:13507296
HTG; HTGS PHASE1.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 219809)
Muse chromosome 4 genomic sequence
I Uppublished
Lo 219809)
Le Chases 1 to 219809
                                                                                                                                                                                                                                                                                                                                                                                                                                            142 LeuGlyAsp------GlyArgSerLeuGlyLeuThrIleArgGlyGlyAlaGluTyr 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .59 GlyLeuGlyIleTyrIleThrGlyValAspProGlySerGluAlaGluGlySerGlyLeu 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 LysValGlyAspGlnIleLeuGluValAsnGlyArgSerPheLeuAsnIleLeuHisAsp 198
                                                                                                                                                                                                                                                                                                                                                                        22 AspargargserThrLeuHisLeuLeuGlnGlyGlyAspGluLysLysValAsnLeuVal 141
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Direct Submission

Submitted (17-JAN-2001) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany

* NOTE: This is a 'working draft' sequence. It currently

* Consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be prestred.
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199454: gap of unknown length
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333531
81
11
39
28
5
   Length:
Matches:
Conservative:
Miswatches:
Indels:
Gaps:
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                                                                                                                                90-151 (1-260) x AC127863
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   2.73e-10
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25.04%
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Similarity:
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Inu Apr 22 UY:45:59 20U4
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51.1120.151.020.0/0.01.85

Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 2.16e-10 330.50 90.36% 81.93% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.: No.:

US-10-078-090-151 (1-260) x AF336379 (1-219809)

1911/2 GTGAATGGGGGGGGGTTTCTCAACATCCTGCATGAGGCAGGGAAGCTGCTCAAGTCA 191113 207 SerArgHisLeuIleLeuThrValLysAspValGlyArgLeuProHisAlaArgThrThr 226 187 ValAsnGlyArgSerPheLeuAsnIleLeuHisAspGluAlaValArgLeuLeuLysSer 206 190992 GGGTCTGGT 190984 247 GlySerGly 249 g 업 g ਨੇ g δ ð ò 8

AC131430 237260 bp DNA linear HTG 15-NOV-2002 Rattus norvegicus clone CH230-133E19, WORKING DRAFT SEQUENCE, 2 unordered pieces. AC111430.3 GI:25007366 HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP. Rattus norvegicus (Norway rat) Rattus norvegicus AC131430/c LOCUS DEFINITION SOURCE ORGANISM ACCESSION VERSION KEYWORDS

Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.

REFERENCE

is Muzny, D. Marie, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, H., Alebrooks, S., Amin, A., Anguiano, D.,
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COMMENT

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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Query Match:
DB:
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2213 bp mRNA linear PRI 02-DEC-1999
Homo sapiens mRNA for autoimmune enteropathy-related antigen
AIE-75, complete cds.
AB018687.1 GI:5231270
autoimmune enteropathy-related antigen AIE-75, AIE-75.
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 ValAspProGlySerGluAlaGluGlySerGly---LeuLysValGlyAspGlnIleLeu 185
                                                                                                                                                        235932 236931: contig of 235931 bp in length 235932 236031: gap of unknown length 236032 237260: contig of 1229 bp in length. Location/Qualifiers
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67
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325.50
89.29$
79.76$
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Best Local Similarity:
Query Match:
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DEFINITION
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1 (sites)
Chobysahi,I., Imamura,K., Kubota,M., Ishikawa,S., Yamada,M.,
Tonoki,H., Okano,M., Storch,W.F., Moriuchi,T., Sakiyama,Y. and
Kobayashi,K.
Identification of an autoimmune enteropathy-related 75-kilodalton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LeuArgArgAlaLysAlaHis---GluGlyLeuGlyPheSerlleArgGlyGlySerGlu
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                                                                                                                                                                                                                                                                     Kobayashi, T.

Kobayashi, T.

Kobayashi, T.

Kobayashi, T.

Kobayashi, Hokkaido University
School of Medicine, Department of Pediatrics; North-15, West-7,

Kita-ku, Sapporo, Hokkaido 060-8638, Japan

(E-mail:ichikoba@med.hokkaia.ac.jp, Tel:011-716-1161,

Fax:011-736-9267)
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                                                                                                                                                                           783 CAGAAGCCIGGCAICTITAICAGCCAIGTGAAACCIGGCITCCCIGICIGCTGCTGAGGGGA 842
                                                                                                                                                                                                          198 AspGluAlaValArgLeuLeuLysSerSerArgHisLeuIleLeuThr---ValLysAsp 216
                                                                                                                                                                                                                                                                             903 AAGGAGGTGTAAAIGIGCTGAAGAGTAGCCGCAGCCTGACCATCTCCATTGTAGCTGCA 962
                                                                                                                                                                                                                                                                                                                217 ValGlyArgLeuProHisAlaArgThrThrValAspGluThrLysTrpIleAlaSerSer 236
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                     137
                                                                      138 yajAsnLeuValleuGlyAspGlyArgSerLeuGlyLeuThrjleArgGlyGlyAlaGlu 157
                                                                                                                        158 TyrGlyLeuGlyIleTyrIleThrGlyValAspProGlySerGluAlaGluGlySerGly 177
98 GlnGlyArgSerIleSerProProSerGlyLeuProGlnProHisGlyGlyAlaLeuArg 117
                                                   118 GlnGlnGluGlyAspArgArgSerThrLeuHisLeuLeuGlnGlyGlyAspGluLysLys
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

; Search time 4115.23 Seconds	(without alignments)	12169.150 Million cell updates/sec
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April		
Run on:		

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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

			Description		BC014524 Homo sapi	BE890168 601513147	BX390092 BX390092	BI732824 603353931
COLUMNICO			ID		BC014524	BE890168	BX390092	471.8 28.1 651 12 BI732824
			8	-	11	10	13	12
			ength	1 1 1 1 1 1	4569	602	908	651
	ф	Query	Match Length DB		44.3	35.9	31.7	28.1
			Score		742.4	602	531.8	471.8
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## ALIGNMENTS

	BC014524 4569 bp mRNA linear HTC 19-NOV-2003	Homo sapiens CASK-intera	IMAGE:3834205), with apparent retained intron.		BC014524.1 GI:17939549	HTC.	Homo sapiens (human)		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,	Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,	Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,	Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,	Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,	Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,	Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,	Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,	Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,	McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,	Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,	Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,	Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,	Sanchez. A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
RESULT 1	LOCUS	DEFINITION		ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS													

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Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

En (bases 1 to 602)

In (bases 1 to 602)

NH-MGC http://mgc.nci.nih.gov/.

Lu Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies (Inc.

CDNA Library Preparation: Life Technologies, Inc.

Clone distribution: MGC. Cone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llh.gov

Plate: LLAM9736 row; m column: 12

High quality sequence stop: 602.
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                                                                                                                                                                                                                                                                                                                                                                                            2182 GTCAGGCTGCTTAAGTCATCTCGGCACCTCATCCTGACAGTGAAGGACGTCGGGAGGCTG 2241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1942 GGTGACCGGAGGAGCACCCCCCCCCCCCCCCAGGAGGGGATGAGAAAAAGGTGAACCTG 2001
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  1882 AGCATCTCCCCACCCTCGGCCTGCCCCAGCCCCACGTGGTGCCCTGAGGCAGCAGGAG 1941
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb.
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                                                                                                                                                                                                                                                                                                                                                         603
                                                                                                                                                                                                                                                                                                                                                                                                                                                             604 GTCAGGCTGCTTAAGTCATCTCGGCACCTCATCCTGACAGTGAAGGACGTCGGGAGGCTG
                                                                                                                                                                               2002 GIGCTGGGGGACGCCCGGTCCCTGGGCCTCACGATCCGTGGGGGAGCTGAGTACGGCCTT
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                                                                                                                                                                                                                                                                                   364 GGTGACCGGAGGAGCACCTGCTCCTGCAAGGAGGGGGATGAGAAAAAAGGTGAACCTG
                                                                                                                                                                                                                                                                                                                                                         544 GGGGACCAGATTCTAGAAGTGAATGGGCGGAGCTTTCTCAACATCCTACACGACGAGGCT
                                                                                                                                                       424 GIGCIGGGGACGGCCGGTCCCTGGGCCTCACGATCCGTGGGGGAGCTGAGTACGGCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2302 ACCAIGGCGAACICGGCAGGGITT 2325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     724 ACCATGGCGAACTCGGCAGGGTCT 747
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Homo sapiens
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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                             Strausberg, R.
Direct Submission
Submission
Submitted (24-SEP-2001) National Institutes of Health, Mammalian
Submitted (24-SEP-2001) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 14 Row: f Column: 19 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
                                                                                                                                                                                                                                                                                                                                                                                                          Outact: MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue progurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Institute for Systems Biology
http://www systemsbiology.org
contact: amadam@systemsbiology.org
Anup Madan, Jessica Fahay, Erih Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGCGGCGTGCCAAGGCCCACGAGGCTTGGGCTTCAGCATCCGTGGGGGCTCGGAGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone has the following problem: retained intron.
Location/Qualifiers
1. .4569
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603353931F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5361582 5',
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/note="list strand cDNA was primed into the Not I and EcoR v
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Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSOBAF042ZH04_AF03969_1. Location/Qualifiers
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Matches 564; Conservative
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E. 1 (bases 1 to 905)
S. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 seqref@genoscope.ons.fr www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5156.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAF042ZH04_AF03969_l&cluster=5156.r.
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                            Pred. No. 2.3e-107;
Mismatches 0;
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbe-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory

Tissue Procurement: The Cepko Laboratory

Tobn Library Arrayed by: The I.M.A.G. E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LiAM11919 row: m column: 07
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 651)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="Images:5361582"
/tissue_type="retina"
/lab_bost="DH10B (phage-resistant)"
/lab_bost="DH10B (phage-resistant)"
/clone_lib="MH1 MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
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Location/Qualifiers
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/mol_type="mrna"
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/clone="IMAGE:661639"
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/note="Organ="Brain; Vector: pYX-Asc; Site_1: BcoR I;
/note="Organ="Brain; Vector: pYX-Asc; Site_1: Bcording
Bonaldo, Lennon and Soares, Genome Research on a 1% agarose
gel. First strand GDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCOAGACAC, This library was created for the University
lows Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Haalth (NIMH), Hemin Chin, Ph.D.,
program coordinator."
                                                                                                                                                                             729 bp mRNA linear EST 09-JUL-2003
UI-MFW0-cbz-b-04-0-UI.rl NIH BWAP_FW0 Mus musculus cDNA clone
CA321445
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (Dases 1 to 79)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The following repetitive elements were found in this cDNA sequence: 146_183, >GC_rich#Low_complexity
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CA321445.1 GI:24539543
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

10 Loases 1 to 693)
NIH-MGC http://mgc.nci.nih.gov/,
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CONTACT: CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Clone distribution: MGC Column 23
High quality sequence stop: 643.

High quality sequence stop: 643.
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602269794F1 NIH_MGC_84 Homo sapiens CDNA clone IMAGE:4358158 5',
                                                                                                                                                                  943 ACACCATCCAACTGTCTTCTTTATTTGTCCCCAAATTACTTAACTCATTCTATAGAC 1002
                                                                                                                                                                                                                                                                                                                                     1063 GATGAAAGAGAGAGAGAGAGAGAAAGAGAGAGAGATGCTTTGGGGTGTATTTGGCCAGAG 1122
                                                                                                                                                                                                                                                                                          121 CITAGTIGCITCATCCAAAAGTGGGGACCATAACCCTGCCCTCATCCCAGATCTGTGCA 180
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                                                                                                                                                                                                61 ACACCATCCAACTGTCTCATTCTTTATTTGTCCCCAAATACTTAACTCATTCTATAGAC
                                                                                                                                                                                                                                                                                                                                                                              181 GATGAAAGAGAGGAAGGGAAAGAGAGAGAGAGAGAGATGCTTTGGGGTGTATTTGGCCAGAG
                                                                                 883 CATGACCTGGGCACATCCCTCTTCTTTGGCCTCAGTTTCCCCATGGAAAGCTGAAAT
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                                             ..
0
  Length 432
                                             Indels
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25.8%; Score 432; DB 9;
100.0%; Pred. No. 4e-74;
ive 0; Mismatches 0
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                               Best Local Similarity 100.0
Matches 432; Conservative
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BF969269
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BF969269
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DKFZp434B1519 r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434B1519, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKR2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No s1 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCATCTCCCCACCTCGGGCCTGCCCCAGCCCCACGTGGTGCCCTGAGGCAGCAGGAGG 364
                                                                                                                                                                                                                                                                                                                                   562 AIGACCGAAGGAGTACCCTCCACCTCCTGCAGAGGAGGAGGAAAAAGGTGAAAAAGGTGAGCTGG 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       681
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                                                                                                                                                                  GCATCCCTGGGGGCTACGTCACCACACCACTTCTACACCTGGGTGGACCCGCAGGGCCGCA 304
                                                                                        GGGTCGGGGACCAGATTCTGCGCGTCAACGACAAATCCCTGGCCCGGGTGACCCACGCGG 184
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
             available.
This clone (DKFZp434B1519) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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                                                                                                                                       /organism="Homo sapiens"
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/moi_type="mRNA"
/do_xref="txxxon:9606"
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/dev_stage="adult"
/dev_stage="Dib="44" (synonym: htes3)"
/clone="Ub="434" (synonym: htes3)"
/note="Vector: pSport1; Site_1: Sall"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                485 GCATTTACATCACTGGCGTGGACCCAGGCTCTGAAGCAGAAGCCAGCG 532
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Unpublished (1999)
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota, Metazoa; Chordata; Sciurognathi; Muridae; Mus.

1 (Dases 1 to 904)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapba-r@mail.nih.gov

Tissue Procurement: Dr. David Rowe and Dr. Mina

CDNA Library Preparation: Invitrogen Corp

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: NDAM0314 row: c column: 15

High quality sequence store: 18

High quality sequence start: 18

High quality sequence start: 18

High quality sequence start: 18
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally; oligo-dT_primed. Average insert size_1.29 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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AGENCOURT 11348497 NIH MGC_164 Mus musculus cDNA clone
IMAGE:30243230 5', mRNA sequence.
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                                                                                                                                                                                                             Score 409.8; DB 10;
Pred. No. 9e-70;
0; Mismatches 22; I
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CB209310.1 GI:28250873
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Best Local Similarity 95.0%;
Matches 434; Conservative
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SOURCE
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TITLE
JOURNAL
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CB209310
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/ Lab host="Laxon:luvyu" (/clone="IMAGE:13643230" / lab host="IMAGE:13643230" / lab host="DH10B (phage-resistant)" (lone="Ibe="NotE:"DH10B (phage-resistant)" / lone="Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI; / note="Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI; / Non-normalized full-length enriched library from pooled mouse embryonic limb, maxilla and mandible, day 10.5 and 11.5 (size selected for the 0.5.1 kb fragments) Cloned directionally, priming method: 05.1 kb fragments) Cloned directionally, priming method: 01.9 kbp. Priming sequence: s'GACTAGTCTAGATCGCGAGCGGCCC(C(T) 3'. Tissue contributed by, David Rowe. Library constructed by ResGen, Invitrogen Corp."
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1 (bases 1 to 325)

1 (bases 1 to 25)

1 (bases 2 to 325)

1 (bases 3 to 325)

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Grupson, A.J., Soares, F., Brettani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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Homo sapiens cDNA, mRNA sequence.
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 337.4; DB 14
Pred. No. 1.3e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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325.3-NN1182-121100-011-g08 NN1182.
BF953476.1 GI:12370751
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.1%;
al Similarity 87.8%;
368; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
Homo sapiens
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/organism="Homo sapiens"

/mol_type="mRNA"

/db_tref="texton:9606"

/dev_stef="texton:9606"

/dev_steg="Adult"

/clone_lib="NN1182"

/clone_lib="nN1182"

/clone_lib="nN1182"

/clone_lib="nno nervous normal; Vector: pucl8; Site_l: Smal;

/note="Organ: nervous normal; Vector: pucl8; Site_l: Smal;

/note="Organ: nervous normal; Vector: pucl8; Site_l: Smal;

/note="Organ: nervous normal; Vector: pucl8; Site_l: Smal;

/note="Organ: nervous normal; Vector: pucl8; Site_l: Smal;

/note="Organ: nervous normal; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,F.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                   Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-NN1182-
121100-011-902&t3=2000-11-12&t4=1)

Seq primer: puc 18 forward

High quality sequence brop: 324.

1. .324
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                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                545 GGGACCAGATTCTAGAAGTGAATGGGCGGAGCTTTCTCAACATCCTACACGACGAGGCTG
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Best Local Similarity 98.1%; Pred. No. 2.3e-49;
Matches 309; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                         forgatism="Homo sapiens"

/mol type="mRNA"

/db Xref="taxon:966"

/dev stage="Adult"

/clone lib="NN1182"

/note="Yogan: nervous normal; Vector: puc18; Site_1: Smal;

Site_2: Smal; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196, 716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under
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mRNA sequence.
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                                                                                                                                                                                                                   This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-NN1182-121100-011-g08&t3=2000-11-12&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 325.
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Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 324)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.
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                                                                                                         Sao Paulo-SP
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                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Pune Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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18.4%; Score 308.4; DB 10;
Best Local Similarity 99.7%; Pred. No. 6e-50;
Matches 309; Conservative 0; Mismatches 1; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      low stringency conditions.
                                                                                                                                                      Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACCACTGTG 684
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AUTHORS
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BF953479
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MEDLINE
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AUTHORS
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/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="texton:9606"
/dev_stage="Adult"
/clone_lib="NN1182"
/clone_lib="NN1182"
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/note="Organ: nervous normal; Vector: puc18; Site_1: Smal;
/note="Organ: nervous normal; Vector: puc18; Site_1: Smal;
/note="Organ: nervous normal; Vector: puc18; Site_1: Smal;
/note="Organ: nervous normal; Vector: puc18; Site_1: Smal;
/note="Organ: nervous normal; Amin-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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1 (Daess 1 to 342)
Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Sarre, M.J., Soares, F., Brentani, R., Reis, L.F., G. Souza, S.J. and Simpson, A.J.
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                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paulo-SP,
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Best Local Similarity 97.8%; Pred. No. 1.2e-48;
Matches 306; Conservative 0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                    GI:12370820
                                                                                                  sapiens (human)
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BEST.
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Tel: +55-11-2704922
Fax: +55-11-270001
Email: saimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=RC3&t2=RC3-NN1182-
121100-011-No6&C3=2000-1112&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
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High quality sequence stop: 343.
Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases 1 to 343)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunscein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
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343 bp mRNA linear EST 22-JAN-2001
RC3-NN1182-121100-011-h06 NN1182 Homo sapiens cDNA, mRNA sequence.
BF953479
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 GAGCACCTGCACCTCCTGCAAGGAGGGGATGAGAAAAAGGTGAACCTGGTGCTGGGGA
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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17.8%; Score 298.6; DB 10; Length
Best Local Similarity 98.7%; Pred. No. 4.9e-48;
Matches 301; Conservative 0; Mismatches 4; Indels
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Homo sapiens
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1. .342
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 342)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       342 bp mRNA linear EST 22-JAN-2001
RC3-NN1182-121100-011-d05 NN1182 Homo sapiens cDNA, mRNA sequence.
BF953472.1 GI:12370747
EST.
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-NN1182-
121100-011-d05&t3=2000-11-12&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stops: 342.
Location/Qualifiers
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                         304 GAGCACCTGCACCTCCTGCAAGGAGGGGATGAGAAAAAAGGTGAACCTGGTGCTGGGGA
                                                                                                                                  244 CGCCCGGTCCCTGGGCCTCACGATCCGTGGGGGGGCTGAGTACGGCCTTGGCATTTACAT
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                                                                                              CGGCCGGTCCCTGGGCCTCACGATCCGTGGGGGGGGTGAGTACGGCCTTGGCATTTACAT
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GAGCACCCTGCACCTCCTGCAAGGAGGGGATGAAAAAAGGTGAACCTGGTGCTGGGGGGA
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/note="Organ: nervous normal; Amini-library was made by cloning products
Site_1: SmaI;
/note="Organ: nervous normal; Amini-library normal; Letters Patent application
No: 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (Bases 1 to 308)
Diasa Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
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Tel: +55-11-27004922
Email: asimpson@loddig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-NN1182-12100-011-h10&t3=2000-11-12&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 308.
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mRNA sequence.
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                                                                                                                                                                       615 TAAGTCATCTCGGCACCTCATCCTGACAGTGAAGGACGTCGGGAGGCTGCCCCATGCCCG 674
                                                                                                                                                                                                       CACTGGCGTGGACCCCAGGCTCTGAAGCAGAAGGCAGCGGGCTCAAGGTTGGGGACCAGAT 218
                                                                              614
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
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                                                                              TCTAGAAGTGAATGGGCGGAGCTTTCTCAACATCCTACACGACGAGGCTGTCAGGCTGCT
                                                                                                      219 TCTAGAAGTGAATGGGCGGAGCTTTCTCAACATCCTACACGACGACGACGACGACGGCTGTCAGGCTGTCA
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Homo sapiens
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1 (bases 1 to 323)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Tel: +55-11-27004922
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-NN1182-121100-012-f04&t3=2000-11-12&t4=1)
Seq primer: puc la forward
High quality sequence stop: 323.
Location/Qualifiers
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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## ALIGNMENTS

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Searched:

Human; breast; cytostatic; cancer; transgenic; gene therapy; vaccine; Human breast specific gene SEQ ID NO 47. ABV83604 standard; cDNA; 667 06-DEC-2002 (first entry) ABV83604;

WO200266605-A2. Homo sapiens. 29-AUG-2002. gene; ss. 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ĸ, 15-FEB-2001; 2001US-0268999P. (DIAD-) DIADEXUS INC.

Description

Salceda S, Macina RA, Sun Y, Liu C; WPI; 2002-713345/77.

The invention relates to human breast specific nucleic acids (I) comprising: (a) a sequence encoding any one of 95 protein sequences (ABP6614-ABP66708); (b) any one of 115 polynucleotide sequences (ABV83558-ABV83672); (c) a molecule that selectively hybridizes to (a) or (b); (d) a molecule having at least 60% sequence identity to (a) or The breast specific nucleic acid molecules, polypeptides and antibodies are useful for identifying, diagnosing, monitoring, staging, imaging and treating breast cancer and non-cancerous disease states in breast tissue. They are also useful for producing transgenic animals and cells and producing engineered breast tissue for treatment and research. The

RESULT 1 ABV83604

14-FEB-2002; 2002WO-US004284.

Cafferkey R;

Karra

Recipon H,

Hu P,

New isolated breast specific nucleic acid molecules and polypeptides, useful for identifying, diagnosing, monitoring, staging, imaging and treating breast cancer and non-cancerous disease states in breast tissue.

Claim 1; Page 170-171; 254pp; English.

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The invention relates to human breast specific nucleic acids (1) comprissing: (a) a sequence encoding any one of 95 protein sequences (ABP666108); (b) a wole of 115 polymucleotide sequences (ABV83558-ABV83672); (c) a molecule that selectively hybridizes to (a) or (b); (d) a molecule acid molecules, polypeptides and antibodies are useful for identifying, diagnosing, monitoring, staging, imaging and treating breast cancer and non-cancerous disease states in breast tissue. They are also useful for producing transgenic animals and cells and producing engineered breast tissue for treatment and research. The transgenic animals are useful as animal model systems used in elaborating the biological function of the polypeptides, studying conditions and/or disorders associated with aberrant expression and in screening for compounds, effective in ameliorating the conditions. The polymucleotides

New isolated breast specific nucleic acid molecules and polypeptides, useful for identifying, diagnosing, monitoring, staging, imaging and treating breast cancer and non-cancerous disease states in breast tissue.

Claim 1; Page 171-172; 254pp; English.

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S, Macina RA, Liu C;

Salceda Sun Y, WPI; 2002-713345/77.

(DIAD-) DIADEXUS INC

14~FEB-2002; 2002WO-US004284. 15-FEB-2001; 2001US-0268999P.

29-AUG-2002

Homo sapiens.

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TCATCCTATCACTACATAGTAGTATAATAATAATATATAGAGAGATACACAGAAAATATA 1445
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5.8e-156;
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Pred. No. 5.8e-
0; Mismatches
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Human; breast; cytostatic; cancer; transgenic; gene therapy; vaccine;

specific gene SEQ ID NO 48

Human breast 06-DEC-2002

gene;

85

standard; cDNA; 1677

ABV83605 ABV83605 361

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                                                                                              1505
                                                          615
                                         555
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evaluating the toxicity of an agent, useful in drug development or in determining toxicological responses to a new drug, by determining the expression of rat toxicologically relevant genes in the test animal in response to the test agent.
                AGACAAGACTAGAGAAACACAGGACAGACAAAACCACGTGAGGAGGAGCAACACCAGA
      TAGAGAAGATAACAGTGTTCTCTATAAAAAAAAAAAACAGCTGCCCTCTCTGCATAGCTTCT
                                          Rat; toxicity study; rat toxic response gene; toxicological response;
drug development; phase-1 rat CT gene; ds.
                                                                                                                                667
                                                                                                                     GGGGCGAACCACATTACCCCACACACGTGAAAAAGCGAGACCAGGGGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 710 BP; 218 A; 148 C; 189 G; 150 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                                                  (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 275; 388pp; English.
                                                                                                                                                                                                                                              Phase-1 Rat CT gene SEQ ID No 686
                                                                                                                                                                                                                                                                                                                                                                                                                       Farr SB;
                                                                                                                                                                                      ABT09598 standard; DNA; 710 BP
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                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                 WO200266682-A2.
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Matches 96,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7737-ABBT30772). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                             Drosophila melanogaster expressed polynucleotide SEQ ID NO 26708.
                                                                                                                                                                                                          developmental biology; cell signalling; insecticide;
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Pred. No. 1.7e-09;
0; Mismatches 12; Indels 0
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     ВP.
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ABL10742 standard; cDNA; 3316
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Best Local Similarity 87.5%;
Matches 84; Conservative
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                                                                                                               (first entry)
                                                                                                                                                                                                                                                  pharmaceutical; gene; ss
                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
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P-PSDB; ABB66639.
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                                                                                                                                                                                                                      Drosophila;
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                                                           ABL10742;
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1 Similarity 75.0 96; Conservative

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08-SEP-2000; 2000US-02314114P.
08-SEP-2000; 2000US-02314114P.
08-SEP-2000; 2000US-023196BP.
14-SEP-2000; 2000US-023196BP.
15-SEP-2000; 2000US-023196BP.
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15-SEP-2000; 200US-0241178BP.
15-SEP-2000; 200US-0241178BP.
15-SEP-2000; 200US-0241178BP.
15-SE
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2000US-0249264P.
2000US-0249265P.
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17-NOV-2000;
17-NOV-2000;
   Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatoropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds
                                                                                                                                  nervous system related polynucleotide SEQ ID NO 7587
                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2000; 2000US-0179065P.
24-FEB-2000; 2000US-0186369P.
24-FEB-2000; 2000US-0186360P.
16-MAR-2000; 2000US-0186360P.
16-MAR-2000; 2000US-0186360P.
19-MAY-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0214886P.
28-JUN-2000; 2000US-0214886P.
11-JUL-2000; 2000US-0216647P.
07-JUL-2000; 2000US-0216890P.
11-JUL-2000; 2000US-0218890P.
11-JUL-2000; 2000US-0218890P.
11-JUL-2000; 2000US-021818P.
11-JUL-2000; 2000US-021818P.
14-JUG-2000; 2000US-021818P.
14-JUG-2000; 2000US-022514P.
14-JUG-2000; 2000US-022514P.
14-JUG-2000; 2000US-0225266P.
14-JUG-2000; 2000US-0225267P.
14-JUG-2000; 2000US-0225267P.
14-JUG-2000; 2000US-0225267P.
14-JUG-2000; 2000US-0225267P.
14-JUG-2000; 2000US-0225267P.
14-JUG-2000; 2000US-0225268P.
14-JUG-2000; 2000US-0225368P.
14-JUG-2000; 2000US-0225369P.
14-JUG-2000; 2000US-0225363P.
14-JUG-2000; 2000US-0225363P.
15-JUG-2000; 2000US-0223934P.
16-SEP-2000; 2000US-0229343P.
16-SEP-2000; 2000US-0229343P.
16-SEP-2000; 2000US-0229343P.
16-SEP-2000; 2000US-0229343P.
16-SEP-2000; 2000US-0229343P.
16-SEP-2000; 2000US-0229343P.
16-SEP-2000; 2000US-0229343P.
16-SEP-2000; 2000US-0229343P.
16-SEP-2000; 2000US-0229343P.
16-SEP-2000; 2000US-0229344P.
16-SEP-2000; 2000US-0229344P.
16-SEP-2000; 2000US-0229344P.
16-SEP-2000; 2000US-0229344P.
16-SEP-2000; 2000US-0229344P.
16-SEP-2000; 2000US-0229344P.
16-SEP-2000; 2000US-0229344P.
16-SEP-2000; 2000US-0231244P.
16-SEP-2000; 2000US-0231244P.
16-SEP-2000; 2000US-0231244P.
16-SEP-2000; 2000US-0231244P.
                                     ABA15256 standard; DNA; 1817 BP
                                                                                                                                                                                                                                                                                                                                                                                      17-JAN-2001; 2001WO-US001334
                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                   23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                           16-AUG-2001
                                                                       ABA15256;
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protein; male sterile plant; viable pollen production;

Fertility restorer protein genomic DNA sequence

fertility restorer protein selection marker; ds; gene

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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and corber cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic and ending aciderofaments, diabetes mellitus, Crohn's disease, cancering and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infections diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed approach of the printed discastion, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 7587; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1817 BP; 552 A; 289 C; 286 G; 690 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA, Barash SC, Ruben SM
                                                        01-DEC-2000; 2000US-0250391P.

01-DEC-2000; 2000US-0251160P.

05-DEC-2000; 2000US-025198P.

05-DEC-2000; 2000US-0256719P.

06-DEC-2000; 2000US-025198P.

06-DEC-2000; 2000US-0251856P.

08-DEC-2000; 2000US-0251868P.

08-DEC-2000; 2000US-0251868P.

08-DEC-2000; 2000US-0251868P.

08-DEC-2000; 2000US-0251869P.
                                                                                                                                                                                                                                                                         2000US-0251990P.
                                                                                                                                                                                                                                                                                        11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-541565/60.
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338 gregergregergregergregetcrececeterrecentatearcatacatagrag 397
                                                                  278 GAGCATGICIGICIGICIGICIGICIGICICICICICICIGIGIGIGIGIGIGIGIGIGIGIGI 337
                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster expressed polynucleotide SEQ ID NO 32036.
                                                                                                                                                                                                                                    83121 TATTAAACTGAATCTAATTTAATGTGTATATATATAAATATAAATTA 83072
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
Query Match
Best Local Similarity 65.3%; Pred. No. 1.6e-08;
Matches 111; Conservative 0; Mismatches 59; Indels 0;
                                                                                                                                                                                                      398 TATAATAATAATATTAGAGAGATACACAGAAAATATATAGAGAAGATAA 447
                                                                                                                                                                                                                                                                                                                           ABL12518 standard; cDNA; 2278
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                                                                                                                                                                                                                                                                                                                             ATATTAGAGAGATACACAGAAAATATATAGAGAAGATAACAGTGTTCTCTATAAAAAA 467
                                                                                                                                                                                                                                                                                                                                                      TITITCTTGAAAAGCCAAGTGTTGATATGATGATGATATTAATCTTATCTATGAAGAG 852
                                                                                                                                                                                              Score 76.6; DB 5; Length 1817; Pred. No. 1.5e-09;
                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD25213/c

ID ADD25213 standard; DNA; 271990 BP.

XX

AC ADD25213;

XX

DT 15-JAN-2004 (first entry)
                                                                                                                            11.5%;
64.2%;
                                                                                                                            Query Match
Best Local Similarity 64.2
Matches 115; Conservative
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pharmaceutical; gene; ss. Drosophila melanogaster

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0; Gaps

The invention comprises the amino acid and coding sequences of isolated fertility restorer proteins. The DNA and protein sequences of the invention are useful for restoring fertility in male sterile planes, such as Brassica napus plants. The DNA and protein sequences of the invention are useful for increasing production of viable pollen in a plant. The DNA and protein sequences are also useful as selection markers to identify transformed plant cells. The present genomic DNA sequence contains coding sequences for fertility restorer proteins of the invention.

Sequence 271990 BP; 89597 A; 47325 C; 46930 G; 88078 T; 0 U; 60 Other;

New nuclear fertility restorer genes, useful for restoring fertility in cytoplasmic male-sterile plants such as Brassica napus plants, or for increasing production of viable pollen in a plant.

claim 1; SEQ ID NO 87; 191pp; English

Cheung

Landry BS,

Formanova N, Dendy C,

Brown GG,

WPI; 2003-221734/21.

(UYMC-) UNIV MCGILL. (DNAL-) DNA LANDMARKS INC.

12-JUL-2001; 2001US-0305026P. 13-JUL-2001; 2001US-0305363P. 30-JUL-2001; 2001US-0308736P.

12-JUL-2002; 2002WO-US022217.

WO2003006622-A2

23-JAN-2003.

Unidentified

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single nucleotide polymorphism; SNP; fish; Salmo salar; Orechromis niloticus; Atlantic halibut; microsatellite; cod; polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut; detection; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                ADD19798 standard; DNA; 667 BP
                                                                                                                                                                                                                                                                                                                                                              1312 TATAATAATTAATGTT 1297
                                                                                                                                                                                                                                                                                                                                               398 TATAATAATAATAT 413
                                               23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 71.3%;
Matches 97; Conservative
                                  23-MAR-2001; 2001WO-US009231
                                                                                   Adams M,
                                                                                                 WPI; 2001-656860/75.
P-PSDB; ABB68415.
                                                                      (PEKE ) PE CORP NY
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       WO200171042-A2
                                                                                                                                      interactions.
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                    27-SEP-2001
                                                                                   Venter JC,
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The present invention describes an isolated nucleic acid (I) comprising a single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid having nucleotide sequence that hybridises to and (ii) a nucleic acid having nucleotide sequence that hybridises to (i), or its complement under highly stringent hybridisation conditions. (I) an isolated oligonucleotide (II) comprising at least of 10 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O. niloticus sNPs, O. niloticus microsatellites Atlantic halibut SNPs, Con polymorphic sites and seabase polymorphic sites, or their complement; (2) a primer pair (II) suitable for use in PCV, comprising two (II) capable of amplifying a nucleotide sequence chosen from S. salar SNPs and, O. niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod niloticus snps, O. niloticus microsatellites, Atlantic halibut SNPs, cod comprising a collection of candidate parent genotype database polymorphis sites, and seabase polymorphis sites, and comparing a candidate parent genotype and one of the candidate parent genotype and one of the candidate parent genotype and one of the candidate parent genotype and one of the candidate parent genotype and one of the candidate parent genotype and one of the candidate parent genotype includes against sample such as family salmonidae, S. salar, Tilapha, O. niloticus, craibbow trout, halibut, salmonidae, S. salar SNPs and O. niloticus applymorthic cod involved from nucleotide sequence of S. salar SNPs and O. niloticus contentifying nucleic acid molecule comparising a polymorphic comparising commands or commands and parent parent commands of sequence in a sample commands or commands and parent such as sample contacting nucleic acid molecule comparises to (II) is useful for executed from nucleotide sequence contacting nucleic acid molecule comparises to (II) derived from nucleotide sequence source and commands and commands and commands and commands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence in a sample, comprising contacting the sample containing nucleic acids with one or more (II) which is derived from 0. niloticus microsatellite, 0. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic sites or seabass polymorphic sites, and identifying a nucleic acid that hybridises to (II). (III) is useful for detecting nucleic acid molecule comprising a microsatellite sequence in sample. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule comprising single nucleotide polymorphism associated with fish, useful for forming PCR primers which are used for detecting single nucleotide polymorphisms in fish nucleic
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                                                                                                                                                                                                                                   [24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 32; SEQ ID NO 433; 233pp; English
                                                                                                                                                                                                                                         Slettan A, Hoyum M, Lingaas
                         L7-JAN-2003; 2003WO-IB000112.
                                                                                   18-JAN-2002; 2002US-0349950P.
16-AUG-2002; 2002US-0404200P.
                                                                                                                                                                                                                                                                                            WPI; 2003-627388/59.
                                                                                                                                                                            (GENO-) GENOMAR ASA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLis176-ABL30511), expressed DNA sequences (ABLis175-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               338 GIGIGIGIGIGIGIGIGIGIGIGICTICTCCTCCTTTCATCCTATCATACTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seabass polymorphic site nucleotide sequence SEQ ID NO:433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2278 BP; 694 A; 498 C; 419 G; 667 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 32036; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                   Li PWD, Myers EW;
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169 GIGIGIGIGIGIGIGIGIGIGIGITCCICAAIGCACATIAGCGGÍAÁTÍATÁGICAGT 110 398 TATAATAATAATTAGAGAGATACA 424 109 AATAACCCTAACGAGAAGAGAGGGACA 83 g à

RESULT

The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a invention also encompasses expression vectors and host cells comprising a cCA nucleic acid, a polypeptide (sapecially an antibody) that specifically binds to the protein, and a biochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using concepenic retroviruses, which insert into the genome of the host organism or random. Many of these do not carry transduced host encogenes or carcinoma fespecially breast cancer, prostate cancer incidence is a direct consequence of the effects of proviral integration into host carcinoma (sepecially breast cancer, prostate cancer, lymphoma or carcinoma (sepecially to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodies are also useful as therapeutic agents and in screening and evaluating drug candidates. The present sequence of the invention. Note: The complete sequence data for this entered and in screening and evaluating drug candidates. The patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at Mouse, murine, carcinoma associated, oncogene, carcinoma, cancer; breast, prostate, lymphoma, leukaemia, cytostatic, gene therapy, drug screening; New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas. Mouse Itk carcinoma associated gene, SEQ ID NO:1319 Claim 1; SEQ ID NO 1319; 245pp; English. 

Sequence 67832 BP; 17054 A; 15504 C; 15824 G; 18278 T; 0 U; 1172 Other; Query Match
Best Local Similarity 83.8%; Pred. No. 3.5e-08;
Matches 83; Conservative 0; Mismatches 16; Indels 0;

338 grgrgrgrgrgrgrgrgrgrgrgrgrgrcrccrcrrrr 376

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The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polymucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypepcides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a mouse gene of the invention. New recombinant nucleic acid, useful for treating carcinomas, lymphomas, cancers, neoplasm, adenocarcinoma, or sarcomas. Sequence 67832 BP; 17054 A; 15504 C; 15824 G; 18278 T; 0 U; 1172 Other; mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas; cancer; neoplasm; adenocarcinoma; sarcoma; gene. Length 67832; Query Match
Best Local Similarity 83.8%; Pred. No. 3.5e-08;
Matches 83; Conservative 0; Mismatches 16; claim 1; SEQ ID NO 367; 2304pp; English BP. ADB72539 standard; DNA; 67832 02-WAR-2001; 2001US-00798586. 23-OCT-2001; 2001US-00004113. 08-NOV-2001; 2001US-00052482. 30-NOV-2001; 2001US-00997722. 20-DEC-2001; 2001US-00034650. 26-DEC-2001; 2001WO-US051291. (first entry) Morris DW, Engelhard EK; (SAGR-) SAGRES DISCOVERY WPI; 2003-239337/23 WO2003008583-A2 Mouse Itk gene 04-DEC-2003 30-JAN-2003 ADB72539 ADB72539

IID ADB7

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61764 GIGIGIGIGIGIGIGIGIGIATGITACCIGAAACTCT 61802 ADC85281 standard; DNA; 67832 BP 01-JAN-2004 ADC85281; RESULT 1: ADC85281 d

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338 grerererererererererererecerererer 376

Gaps

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16; Indels

Cytostatic; gene therapy, vaccine; cancer; carcinoma-associated gene; CA; secreted; transmembrane; intracellular; ds.

Mouse Itk genomic sequence.

RESULT 10

useful

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The invention relates to a nucleic acid array, where each coordinate contains a single nucleic acid species having one of 770 nucleotide sequences (appearing as ABS76747-ABS77516) as of a Xenopus embryonic gene product, or its complement or hybridisable fragment of not less than 20 contiguous nucleotides of one of those sequences. Also included are detecting differential expression of embryonic genes, comprising in a nucleic acid array comprising genes expressed in embryonic contacting a nucleic acid array comprising genes expressed in embryonic but not mature cells with nucleic acids from sample and control cells; and cletecting differential hybridisation of nucleic acids from the sample cells relative to the control cells; and detecting defects in care contacting nucleic acids from test cells undergoing development with a nucleic acid array of gene products known to play a fundamental role in the development process; and (b) detecting a difference in expression of a fundamental gene in the sample cells relative to a standard. The invention is useful to identify genes involved in embryonic development and related processes such as cell differentiation. This would be useful for diagnosing developmental contacting and for identifying different types of embryonic cells. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441 cirrangaaracargiraaaaaaaaacaaragirgigigigigigigigigigigigigigigi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 ccrediteccaccideccaaracacrecagaccargrererererererererereres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stellite artificial chromosome; minichromosome; euchromatin; neo-chromosome; necentromere; gene therapy; pericentromeric heterochromatin; ribosomal DNA complete repeating unit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence is one of the 770 Xenopus embryonic cDNA sequences
           Nucleic acid array containing Xenopus embryonic nucleic acids is to identify genes involved in embryonic development, to identify different types of embryonic cells, and to diagnose developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 742 BP; 233 A; 170 C; 107 G; 213 T; 0 U; 19 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds; human; mammalian artificial chromosome; SATAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 73.2; DB 6;
Pred. No. 8.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ribosomal DNA complete repeating unit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                        Claim 1; Page 18; 823pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-00629822.
96US-00682080.
96US-00695191.
97US-00835682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA14747 standard; DNA; 42998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAR-2001; 2001US-00799462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-NOV-2000; 2000US-00724693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.0%;
76.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 76.3 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HADL/) HADLACZKY G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2002160970-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-1996;
15-JUL-1996;
07-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA14747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381
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Best Local &
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                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a recombinant nucleic acid comprising a nucleotide sequence selected from any of the fully defined carcinoma-associated (CA) genes from the 50 tables given in the specification. The CA proteins are secreted, transmembrane or intracellular proteins. The recombinant nucleic acids are useful for screening for drug candidates for diagnosing or treating carcinomas. Sequences given in ADC85215-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 67832 BP; 17054 A; 15504 C; 15823 G; 18278 T; 0 U; 1173 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               embryonic development; developmental disorder; microarray;
                                                                                                                                                                                                                                                                                                                                 New recombinant nucleic acid comprising a nucleotide sequence of ar
the carcinoma-associated (CA) genes, useful for screening for drug
candidates for diagnosing or treating carcinomas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIGTGTGTGTGTGTGTGTGTGTCTCCTCACTCTTT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 73.4; DB 9;
Pred. No. 3.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for diagnosing or treating carcinomas. Sequer
ADC85514 represent CA genes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Frog embryonic gene sequence Q9922010
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 67; 983pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Altmann CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABS76748 standard; cDNA; 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JUL-2001; 2001US-00910943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0219658P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.0%;
83.8%;
                                                                                                                               02-DEC-2002; 2002WO-US038582
                                                                                                                                                                       30-NOV-2001; 2001US-00997722
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Best Local Similarity 83.8
Matches 83; Conservative
                                                                                                                                                                                                                                                     Engelhard EK;
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                                                                                                                                                                                                               (SAGR-) SAGRES DISCOVERY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        differentiation.
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                                                                                                                                                                                                                                                                                                  WPI; 2003-513603/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2002081610-A1
                                                 WO2003045230-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kenopus laevis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUN-2002.
                                                                                         05-JUN-2003
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cell diffe
                                                                                                                                                                                                                                                          Morris DW,
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365

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Length 742;

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ABS65032 standard; DNA; 42999
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                                                                                                                                                                                                                                     15-DEC-2000; 2000US-00738630
      Hadlaczky G, Szalay AA;
                                                                                                                                                                                                                                                          WPI; 2002-636544/68
             WPI; 2003-238236/23
                                                                                                            Local Similarity
les 84; Conserv
                                                                                                                                                                                                                WO200259370-A2.
                                                                                                                                                                                                                                                   Greenspan RJ,
                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                            15-NOV-2002
                                                                                                                                                                                                                       01-AUG-2002
                                                                                                                                     343
                                                                                                                                                                     ABS65032;
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                                                                                                         Query Match
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The present invention relates to a method of identifying a compound that modulates attention deficit hyperactivity disorder (ADHD) in a mammal. The method comprises administering a test compound to an invertebrate, and measuring a foraging behaviour of the invertebrate, where the compound that modulates the foraging behaviour of the invertebrate is characterised as a compound that modulates ADHD in a mammal. The compound identified by the new method of the invention is useful for diagnosing or treating ADHD, hypertension or other diseases associated with a nitric oxide/cGMP-dependent protein kinase network in a mammal, particularly humans. The method distinguishes a compound that has a specific effect on ADHD, hypertension or other diseases associated with a nitric oxide/cGMP-dependent kinase protein network in a mammal from a compound that has a non-specific effect. The present sequence represents a DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated substantially pure plant satellite artificial chromosome useful for producing transgenic plant, producing gene product, cloning centromere from plant.
Identifying a compound that modulates an attention deficit hyperactivity disorder (ADHD) for treating e.g. ADHD or hypertension, comprises measuring a foraging behavior an invertebrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome; SATAC; transgenic; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 42999 BP; 6411 A; 13605 C; 11491 G; 11479 T; 0 U; 13 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 73.2; DB 6; Length 42999; Pred. No. 3.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                     associated with invertebrate foraging behaviour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ribosomal DNA (rDNA) repeat region.
                                                                                              Page 182-195; 246pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD61411 standard; DNA; 42999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1996; 96US-00682080.
07-AUG-1996; 96US-00695191.
10-APR-1997; 97US-00835682.
28-NOV-2000; 2000US-00724726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-2002; 2002US-00287313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-00629822
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1 Similarity 82.4%;
84; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               centromere; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Satellite artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-777325/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HADL/) HADLACZKY G. (SZAL/) SZALAY A A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2003101480-A1.
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15-JUL-1996;
07-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD61411;
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                                                                                                                                                                                                                                                                                            The invention relates to preparing cells or cell lines comprising introducing a mammalian artificial chromosome that a comprises a nucleic acid encoding a therapeutic product or a gene product into a cell or tissue of a host animal. The artificial chromosome is a mammalian SATAC (satellite artificial chromosome) or a minichromosomes based on the method is useful for preparing cells or cell lines, which may be employed in cell-based methods for production of heterologous proteins, gene therappy, or generation of transgenic non-human animals. The cells or cell lines are also useful for cell fusion, as recipient cells for donor DNA encoding a gene or multiple genes, or for delivery of heterologous DNA into cells. The present sequence is the Human ribosomal DNA complete repeating unit, useful for taxing artificial chromosomes to perior perior perior perior perior man animal chromosomes to perior perior manner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  renergrenergrenergrenergrenergrenergrenergrenergrenergrenerg
                                                                                                                                  Preparing cells or cell lines for use in cell-based methods for heterologous protein production or gene therapy, by introducing a minichromosome or a mammalian satellite artificial chromosome into a cell or tissue of a host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Attention deficit hyperactivity disorder; ADHD; hypertension; invertebrate foraging behaviour; nitric oxide; hypotensive; cGMP-dependent protein kinase; human; neuroleptic; ds; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 42998 BP; 6410 A; 13612 C; 11484 G; 11479 T; 0 U; 13 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Invertebrate foraging behaviour associated human DNA sequence #12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 42998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTGTGTGTGTGTGTGTCTCCTCACTCTTTCATCCTAT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 73.2; DB 7;
Pred. No. 3.4e-08;
0; Mismatches 18;
                                                                                                                                                                                                                                                             Disclosure; Page 76-95; 109pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NEUR-) NEUROSCIENCES RES FOUND INC.
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82.4%;
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            (SZAL/) SZALAY A A.
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Example 6; Page 76-94; Opp; English.
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ö The present invention relates to novel pure plant satellite artificial chromosome (SATARC). Sequences of the invention are useful for producing transpenic plants and gene products. They are also useful for cloning a centromere from a plant. The present sequence is human ribosomal DNA (rDNA) repeat region used in the exemplification of the invention Query Match
Best Local Similarity 82.4%; Pred: No. 3.4e-08;
Matches 84; Conservative 0; Mismatches 18; Indels 0; Gaps Sequence 42999 BP; 6411 A; 13605 C; 11491 G; 11479 T; 0 U; 13 Other; රු පු

Search completed: April 21, 2004, 21:35:59 Job time : 267.231 secs

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Thu Apr 22 09:46:01 2004
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April 21, 2004, 21:08:41; Search time 280.003 Seconds (without alignments) 10740.063 Million cell updates/sec
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| cgn2 6/prodata/1/pubpna/US07 PUBCOMB.seq:*
| cgn26/prodata/1/pubpna/PCT NEW PUB.seq:*
| cgn26/prodata/1/pubpna/US06 NEW PUB.seq:*
| cgn26/prodata/1/pubpna/US06 NEW PUB.seq:*
| cgn26/prodata/1/pubpna/US07 NEW PUB.seq:*
| cgn26/prodata/1/pubpna/US07 NEW PUB.seq:*
| cgn26/prodata/1/pubpna/US08 PUBCOMB.seq:*
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| cgn26/prodata/1/pubpna/US08 PUBCOMB.seq:*
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| cgn26/prodata/1/pubpna/US09 NEW PUB.seq:*
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| cgn26/prodata/1/pubpna/US10B_PUBCOMB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10-0 , Gapext 1.0
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667
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 47, Appl.
Sequence 285026,
Sequence 285026,
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Sequence 285028,
Sequence 285027,
Sequence 19, Appl.
Sequence 17, Appl.
Sequence 87, Appl.
Sequence 26, Appl.
Sequence 26, Appl. Description Sequence US-10-027-632-285026 US-10-027-632-285028 US-10-027-632-285028 US-10-027-632-285027 US-10-027-632-285027 US-10-027-632-285027 US-10-087-192-19 US-10-087-192-1864 US-10-087-192-262 US-10-087-192-262 US-10-087-192-1864 US-00-997-722-67 SUMMARIES Б Query Match Length DB 11.4 113633 11.3 271990 11.3 271990 11.2 271990 11.2 53954 11.0 67832 Result υυυυ

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US-10-175-523-87	-09-910-943-	9-799-46	US-09-836-911	US-09-738-630	US-10-125-	US-10-151-081	US-10-287-313-	US-10-219-6	US-10-027-632-	US-10-027-6	US-10-027-632-903	US-10-027-632-3173	US-10-087-192-18	US-10-085-117-325	US-10-087-1	US-10-087-192-183	US-10-087-192-143	US-10-085-117-2	US-10-229-8	-771-208-2	US-09-864-761-2623	39-864-761-	US-10-087-192-1		US-10-087-192-2	US-10-026-188	US-10-126	-10-126-912	-10-126-912	US-10-087-192-1993
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73.4	73.2	73.2	73.2	73.2	73.2	73.2	73.2	73.2	72.8	72.8	72.8	72.8	72.8	72.6	72.6	72.4	72.2	72.2	72.2	72.2	71.8	71.8	71.8	71.6	71.6	71.2	71	71	71	71
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## ALIGNMENTS

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Sequence 47, Application US/10078090

Sequence 47, Application US/10078090

Publication No. UG20030044815Al

GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Raize, Rabana
APPLICANT: Raize, Rabana
APPLICANT: Raize, Rabana
APPLICANT: APPLICANT: Cafferkey, Robert
APPLICANT: Diu, Chenghua
APPLICANT: Diu, Chenghua
APPLICANT: Biu, Chenghua
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CORGANISM: Homo sapien
US-10-078-090-47
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                                   APPLICANT: Wang, David G.

JITLE OF INVENTION: Identification and Mapping of Single Nucleotide
JITLE OF INVENTION: Identification and Mapping of Single Nucleotide
JITLE OF INVENTION: POLYMOTOPHISMS in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/11/027,632
CURRENT FILING DATE: 2002.04-30
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-39
PRIOR FILING DATE: 1900-03-29
PRIOR PELING DATE: 1900-03-29
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-09-11-23
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-18
PRIOR FILING DATE: 1999-09-19
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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           16 GAGGICCAIAACCCIGCCICCAICCCCAGAICTGCAGAIGAAAGAGAGGGAGGGAGAAG
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APPLICANT: Salceda, Susana
APPLICANT: Salceda, Roberto
APPLICANT: Hu, Ping
APPLICANT: Hu, Ping
APPLICANT: Hu, Ping
APPLICANT: Karra, Kalpana
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
FILE REPERBURCE: DEV. 2012-02-14
PRIOR PILING DATE: 2002-02-14
PRIOR PILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PATENTIN Version 3.1
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                                   GCTGGATCCCATGAAGAATCTGGGTGAGAGGGTCTTAAAGTCATAAACTGAGATCCAGT
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97.0%; Score 647.2; DB 15; Length 1677;
Best Local Similarity 99.5%; Pred. No. 4.1e-171;
Matches 649; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 48, Application US/10078090 Publication No. US20030044815A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CRGANISM: Homo sapien
US-10-078-090-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGGAGA 667
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LENGTH: 1677
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                                                                                 Length 553;
                                                                                 Score 76.6; DB 13; Length
Pred. No. 4.5e-11;
0; Mismatches 64; Indels
                                                                                                                                       289 rerererererererererererer
                                                                                                                                                                                                                                                                                                                                          Sequence 285028, Application US/10027632 Publication No. US20020198371A1 GENERAL INFORMATION:
                                                                                  11.5%;
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Best Local Similarity 64.2
Matches 115; Conservative
                                                                                 Query Match
Best Local Similarity 64.2'
Matches 115; Conservative
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; ORGANISM: Human
US-10-027-632-285028
                                                                                                                                                                                                                                                                                                                    RESULT 4
US-10-027-632-285028
                             ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-285026
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LENGTH: 553
    SEQ ID NO 285026
LENGTH: 553
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; Sequence 285028, Application US/10027632
; Publication No. US20030204075A9
; Publication No. US20030204075A9
; Greekal Invervation:
    APPLICANT: Wang, David G.
    TITLE OF INVERVION: Polymorphisms in the Human Genome
    TITLE OF INVERVION: Polymorphisms in the Human Genome
    FILE REPERENCE: 108027.129
; CURRENT PILING DATE: 2002-04-30
; PRIOR PILING DATE: 2000-07-12
; PRIOR PILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-11-23
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GENERAL INVENTION:

APPLICANT:
Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: POLYMORPHISMS in the Human Genome
FILE REFERENCE: 106827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US/02/03/06

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/195,483

PRIOR APPLICATION NUMBER: US 60/195,358

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

SERO ID NOS: 325720

SERO ID NO 265026

LENGHH: 553

LENGHH: 553

LENGHH: 553
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; Sequence 285026, Application US/10027632; Publication No. US20030204075A9; GENERAL INFORMATION:
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Best Local Similarity 64.2%;
Matches 115; Conservative
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; ORGANISM: Human
US-10-027-632-285027
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Sequence 285027, Application US/10027632

Publication No. US20020198371A1

JGENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 10827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2000-04-30

PRIOR PELING DATE: 2000-04-20

PRIOR PELING DATE: 2000-04-20

PRIOR PELING DATE: 2000-04-20

PRIOR PELING DATE: 2000-04-20

PRIOR PELING DATE: 2000-03-29

PRIOR PELING DATE: 2000-03-29

PRIOR PELING DATE: 2000-03-29

PRIOR PELING DATE: 2000-03-24

PRIOR PELING DATE: 2000-03-24

PRIOR PELING DATE: 1999-01-23

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR PELING DATE: 1999-01-23

PRIOR PELING DATE: 1999-01-23

PRIOR PELING DATE: 1999-00-08

PRIOR FILING DATE: 1999-08-08

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FREEESE FEETER FILING DATE: 1999-08-08

LENGTH: 553
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Best Local Similarity 63.7%; Pred. No. 5.8e-11;
Matches 114; Conservative 1; Mismatches 64; Indels
                                                                                                                                                                                                                                           Query Match
11.5%; Score 76.6; DB 16; Length
Best Local Similarity 64.2%; Pred. No. 4.5e-11;
Matches 115; Conservative 0; Mismatches 64; Indels
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 285028
LENGTH: 553
                                                                                                                                                ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-285028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-285027
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                                                                                                        Query Match 11.4%; Score 76.2; DB 13; Length 113633; Best Local Similarity 96.3%; Pred. No. 1e-09; Matches 78; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                398 TATAATAATAATATTAGAGAGATACACAGAAAATATATAGAGAAGATAA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
11.3%; Score 75.6; DB 15;
Best Local Similarity 65.3%; Pred. No. 2.4e-09;
Matches 111; Conservative 0; Mismatches 59;
                                                                                                                                                           NAME/KEY: modified base
LOCATION: (144241)...(144300)
OTHER INFORMATION: a, t, c, g, other or unknown
                                                                                                                                                                                                                        45422 TGTGTGTGTGTGTGTGTGT 45442
                                                                                                                                                                                                           343 TGTGTGTGTGTGTGTGT 363
                                            NAME/KEY: misc_feature

) LOCATION: (1)...(113633)

) OTHER INFORMATION: n = A,T,C or G

US-10-087-192-19
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ORGANISM: Raphanus sativum
           TYPE: DNA ORGANISM: Mus musculus
LENGTH: 113633
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                                                                                                                                                                                                                           405 ATAAATATTAGAGAGATACACAGAAAATATATAGAGAAGATAACAGTGTTCTCTATAAAA 464
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                                                                                                         Score 74.6; DB 13; Length 53954;
Pred. No. 1.9e-09;
0; Mismatches 19; Indels 0;
                                                                                                                                                                                                                                                                                                             329 renerereregiqiqiqiqiqiqiqiqiqiqiqiqicrccrcacrc 373
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US-10-087-192-1864/c
| US-10-087-192-1864/c
| Sequence | 1864, Application US/10087192
| Sequence | 1864, Application US/10087192
| Sequence | 1864, Application US/2002182586A1
| GENERAL INFORMATION:
| APPLICANT: Engelhard, Eric K. |
| APPLICANT: Engelhard, Eric K. |
| TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR ITLE OF INVENTION: NOVEL COMPOSITION AND METHODS FOR CURRENT PAPLICATION NUMBER: US/10/087,192 |
| CURRENT PILING DATE: 2002-03-01 |
| PRIOR FILING DATE: 2000-12-22 |
| PRIOR FILING DATE: 2000-12-22 |
| PRIOR FILING DATE: 2001-03-02 |
| NUMBER OF SEQ ID NOS: 2059 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| IBNGTH: 350764
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                                                                                                             Query Match
Best Local Similarity 81.9%;
Matches 86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CRGANISM: Homo sapiens
US-10-087-192-1864
                                   TYPE: DNA
CORGANISM: Homo sapiens
US-10-087-192-262
SEQ ID NO 262
LENGTH: 53954
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                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (26053)..(26112)
OTHER INFORMATION: "n" at positions 26053 through 26112 can be any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.0%; Score 73.4; DB 12; Length 67832; 83.8%; Pred. No. 4.8e-09; ive 0; Mismatches 16; Indels 0;
APPLICANT: Morris, David

APPLICANT: Engelhard, Eric

IIILE OF INVENTION: WOUEL COMPOSITIONS AND METHODS FOR CANCER

IIILE OF INVENTION: WOUEL COMPOSITIONS AND METHODS FOR CANCER

FILE REFERENCE: A-71171/RMS/DCF

CURRENT APPLICATION NUMBER: US 09/747,377

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-12-22

PRIOR PELLING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 301

SOFTWARE: PARCHIN VERSION 3.1

SEQ ID NO 67

LENGTH: 67832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (28892)..(29324)
OTHER INFORMATION: "n" at positions 28892 through 29324 can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (57867)..(57886)
OTHER INFORMATION: "n" at positions 57867 through 57886 can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEX: misc_feature
LOCATION: (60656)..(60675)
OTHER INFORMATION: "n" at positions 60656 through 60675 can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (43840)..(43859)
OTHER INFORMATION: "n" at positions 43840 through 43859 can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (30179) ..(30757)
OTHER INFORMATION: "n" at positions 30179 through 30757 can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (32761)..(32780)
OTHER INFORMATION: "n" at positions 32761 through 32780 can
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Publication No. US20030096264A1
GENERAL INFORMATION,
APPLICANT: Brockman, Jeffrey
APPLICANT: Evans, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Evans, David
Hook, Derek
Klimczak, Leszek
Laeng, Pascal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (43840)..(43
                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-175-523-87/c
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APPLICANT:
APPLICANT:
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RESULT 14
US-09-997-722-67
Sequence 67, Application US/09997722
Publication No. US2046072154A1
GENERAL INFORMATION:

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us-10-078-090-47.rnpb
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37062 GIGICIGIO INTITITI INTITITI INTITITI INTITICACCATATACATTGATGTAAG 37003
                                                                                                                                                                                                                                              0; Gaps
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Best Local Similarity 70.5%; Pred. No. 6.8e-09;
Matches 98; Conservative 0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                                     Search completed: April 22, 2004, 01:59:50 Job time : 287.003 secs
                                                                                                                                                                                                                                                                                                                              37002 rererrahrecaarecada 36984
                                                                                                                                                                                                                                                                                                                398 TATAATAATAATAGA 416
                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-175-523-87
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Title: Perfect score:

Sequence:

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Searched:

Database :

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432 bp mRNA linear EST 04-SEP-2003
DKF2p434B1519 rl 434 (synonym: htes3) Homo sapiens cDNA clone
DKF2p434B1519, mRNA sequence.
      AX897298 RPCT-24-1
BX151392 Danic rer
CA581263 ESTOG0338
BX146272 Danio rer
BH350473 CH230-120
AL274417 Tetracdon
BH383838 AG-ND-119
BH383838 AG-ND-119
CC775881 CH240_130
CC775881 CH240_130
AL973430 Danio rer
AQ780204 170006872
AL168930 Tetracdon
BX242790 Danio rer
AQ780204 HS 3138 B
AL733910 Danio rer
BX182339 Danio rer
BX1823372 CH230-444
BX23372 CH230-444
BX23372 CH230-281
BX240451 Danio rer
BX19552 CH230-281
BX23352 CH230-281
BX235248 1M0065D11
AX2973484 2M0247819
AX2973484 2M0247819
AX3973616 RPCI-23
BX10556 CAG120-150
BX105188 CH230-150
BX105188 CH230-150
BX105188 CH230-150
BX105188 CH230-150
BX105188 CH230-150
BX105188 CH230-150
BX10518 CH230-150
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BX10518 CH230-150
BX10518 CH230-150
BX10518 CH230-150
BX10517 Danio rer
AL193282 Tetracdon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Injoistaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKPZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No s1 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 432)
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This clone (DKF2p434B1519) is available at the R2PD in Berlin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                  BZ233672
BZ233672
BZ240451
AL514869
AL514819
AZ373484
AZ335248
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BZ105168
BX404043
CB937318
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CC080479
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Unpublished (1999)
Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL049078.1 GI:4728387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
Homo sapiens
                                 Wiemann,S.
EST (Otter
                                             AL049078
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AL049078
LOCUS
DEFINITION
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KEYWORDS
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JOURNAL
COMMENT
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AUTHORS
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AL514829 AL514829
AZ997081 2M0283C01
BZ271973 CH230-275
                                                                                April 21, 2004, 21:05:04; Search time 1636.77 Seconds (without alignments) 12169.150 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                         1 gogtggtcgcggcccgaggt.....aagcgagaccagggggggaga
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                27513289 segs, 14931090276 residues
                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AL514829
AZ997081
BZ271973
                                                            - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
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667
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1246
627
752
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em_gss_f
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13.3
13.2
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284.2 88.6 87.8 87

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Score

No.

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Score 88.6; DB 9;
Pred. No. 1.1e-07;
0; Mismatches 74;
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Insert Length: 10000 Std Error: 0.00
Plate: 0283 row: C column: 01
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 627.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="UUGC2M0283C01"
/sex="Female"
'db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ997081.1 GI:13868308
                                                                                                                                                                                                                       Query Match
Best Local Similarity 64.3%;
Matches 133; Conservative
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Fax: 801 585 7177
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KEYWORDS
SOURCE
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AZ997081/c
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AUTHORS
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1 (Dases 1 to 1246)

2 ii, W.B., Gruber, C., Jessee, J. and Polayes, D.

1 Unpublished (2001)

2 On Feb 13, 2001 this sequence version replaced gi:12778322.

3 Contact: Genoscope Genoscope Genoscope. Centre National de Sequencage

3 D 191 91006 ENY cedex - France

3 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

3 Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4382.r For more information about this, cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL514829 Homo sapiens NEUROBLASTOWA Homo sapiens cDNA clone CO0550142F05 3-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.genoscope.ons.fr/
cgi-bin/cluster.cgi?seq=CLOBB014ZF05FP1&cluster=4382.r. Contact :
Feng Liang Email : filang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBB014ZF05FP1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 GAAATCTGGGTGAGAGGGTCTTAAAGTCATAACTGAGATCCAGTTGCCAGGTGGCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 TAGTIGCCAACAGIGIAATGIGICACCITITIGAICTICAICAAAATCICAGGCCIGGIGG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324 TAGTTGCCAACAGTGTAATGTGTCACCTTTTGATCTTCATCAGAAATCTCAGGCTGGTGG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                       203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAAGAGAGAGATGCTTTGGGGTGTATTTGGCCAGAGGCCACCAGGCTGGATCCCATGAA 135
                                                                                                                                                                                                                                                                                                                                                                                                 75
  Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 GAAAGAGAGAGATTIGGGGTGTATTTGCCCAGAGGCCACCAGGCTGGATCCCATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                       144 goggaccaraaccergecercareceagarergreeagargaaagagagggaggg
                                                                                                                                                                                                                                                                                                                                                                                               136 GABATCTGGGTGAGAGGGTCTTABAGTCATABACTGAGATCCAGTTGCCAGGTGGCTGCA
                                                                                                                                                                                                                                                                                                                                                            Gaps
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/db xref="taxon:9606"
/clone="mypp="testis"
/dev stage="adult"
/lab_host="bH108"
/clone lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: Sall"
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                                                                                                                                                                                                                                                                                                                42.6%; Score 284.2; DB 9; Length llarity 99.0%; Pred. No. 3.4e-46; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                        organism="Homo sapiens"
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                                                                      1. 432
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Matches 286;
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                                                                                                                                                                                                                                                                                                                        Query Match
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KEYWORDS
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AL514829/c
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AUTHORS
TITLE
JOURNAL
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/cione="CLOBB0142F05"
/cione="CLOBB0142F05"
/cione lib="Homo sapiens NEURBLASTOWA"
/clone lib="Homo sapiens NEURBLASTOWA"
/note="Vector: pCMVSPORT_6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and BCRV sites of the pCMVSPORT 6 vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ997081
2M0283C01R Mouse 10kb plasmid UUGC2M library Mus musculus genomic close UUGC2M0283C01 R, genomic survey sequence.
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Mus musculus
Mus macalus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 627)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      386 ATTACATAGTAGTATAATAATAATATTAGAGAGATACACAGAAAATATATAGAGAAGAT 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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62
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| corganism="Rattus norvegicus"
| mol type="genomic DNA"
| strain="BN/SSNH8d/MCW"
| db_xref="taxon:10116"
| clone="CH230-275L23"
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AL663389.1 GI:18130296
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/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note=="Vector: PWD42nv; Purified genomic DNA from M
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was bydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil #722114|gp|ART29072.1); a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coll XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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CH230-275L23.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone CH210-275L23, genomic survey sequence.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other GSSS: CH230-275L23. TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
The Institute for Genomic Research
Tel: 301 838 0208
Fax: 301 838 0208
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Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
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Best Local Similarity 62.6
Matches 137; Conservative
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availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Plate: 275 row: L column: 23 Seg primer: T7 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.

    (bases 1 to 715)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITICITITITAAAAAAGATITIATATATIGTATGTATATGAGTACACTGCAGAGTCTTC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL663389 ALrectional larval cDNA library Ciona intestinalis cDNA clone 0082D03 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                 /sex="Female"
/cell type="Brain"
/clone lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
FORT-230 Rat (BN/SSNHsd/MCW) BĀC library produced by
Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 rerererererererererererecececerereeerereeererererererererer
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Unpublished (2002)
Contact: Genoscope
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Danjo rerio (zebrafish)

ENALOPICATA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

El (bases 1 to 628)

Rumphray, S.J.; Huckle, E. and Durham, J.L.

Direct Submission

Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished

This sequence was generated from the SP6 end of BAC 111D24

is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:

http://www.sanger.ac.uk/Projects/D_rerio/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BX151392 628 bp DNA linear GSS 28-JAN-2003
Danio rerio genomic clone DKEY-111D24, genomic survey sequence.
BX151392
BX151392.1 GI:27982876
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                                                                                                       Length 492;
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llarity 63.2%; Pred. No. 1e-06;
Conservative 0; Mismatches 75; Indels
                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                        206 ratrcanaritraaaaaacaaataaaararaacarcacar 164
                                                                                                                                           . 64
                                                                                                     Score 84.6; DB 28;
Pred. No. 8.4e-07;
0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-111024"
/tissue_type="Testis"
/note="Vector pindigoBAC-536"
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                                                                                                         12.7%;
69.9%;
                                                                                                             Query Match
Best Local Similarity 69.9
Matches 114; Conservative
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Matches 129; Conserv
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Nouse BAC End Sequences from Library RPCI-24

Unpublished (1999)

Other GSSs: RPCI-24-186D20.TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0208

Email: schaocetigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC

library availability, please contact Pieter de Jong

(pdejongemail.cho.org). Clanes may be purchased from BACPAC

Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end

page: http://www.chori.org/bacpac/orderingframe.htm).

Plate: 186 row: D column: 20

Seq primer: SAC
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/clone lib="RPCI-24"
/note="Vector: pTARBAC1; Site 1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS 05-MAR-2001
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                                                                                                                                                                                                                                                                                                                                     403 TAATAAATATTAGAGAGATACACAGAAAATATATAGAGAAGATAACAGGTATCTCTATAA 462
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RPCI-24-186D20.TJ RPCI-24 Mus musculus genomic clone
RPCI-24-186D20, genomic survey sequence.
AZ897298
                                /clone="0082D03"
/clone lib="directional larval cDNA library"
/note="Vector: pBluescript2SK+"
                                                                                                                                 Length 715;
                                                                                                                                                                            65; Indels
                                                                                                                                   13.0%; Score 86.6; DB 9;
llarity 65.8%; Pred. No. 3.1e-07;
Conservative 0; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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strain="C57BL/64"
/db_xref="taxon:10090"
/clone="RPCI-24-186D20"
/sex="Male"
                   db_xref="taxon:7719"
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Mus musculus
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                                                                                                                                                           Similarity
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Matches 125;
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                                                                                                                                         Query Match
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AZ897298/c
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Autaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

Cypriniformes; Cyprinidae; Danio.

Humphras; S.J., Huckle, E. and Durham, J.L.

Direct Submission
Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambidgeshire, CBIO 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 104G8. 104G8 is part of the Daniokey BAC Library created by R. Plasterk and N.V.

Keygene, Further details;
                                                                                                                                                                                                                                                GSS 13-MAR-2003
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
560 AAGACTAGAGAAAACACAGGACAGGGACAAAAACCACGTGAGGGAGCAACACCAGAGGGG 619
                                          BH350473 TVC CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-120K23, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BX146272 737 bp DNA linear GSS 13-MAF
Danio rerio genomic clone DKEY-104G8, genomic survey sequence
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1 (bases 1 to 796)
2hao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
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                                                                                                                                     837
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Pred. No. 2.1e-06;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/Projects/D_rerio/
location/Qualifiers
1. 737
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-10498"
                                                                                            620 CGAACCACATTACCCCACACGTGAAAAAGCGAGACCA
                                                                                                                                  799 AGACAGAAAGAGGGAAAGCGAAGTCAAAAAAAAAGAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Testis"
/note="vector_pindigoBAC-536"
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Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                     BX146272.1 GI:27977635
                                                                                                                                                                                                                                                                                                                                                             Danio rerio (zebrafish)
Danio rerio
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Best Local Similarity 72.3%;
Matches 107; Conservative 0
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BH350473/c
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BX146272/C
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Paracoccidioides brasiliensis

Bukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; mitosporic Onygenales; Paracoccidioides.

1 (bases 1 to 851)

1 (bases 1 to 851)

1 (bases 1 to 851)

Torres; F.A.G.: Andrade, R.V., Silva, S.P., Maranhao, A.O.,

Torres; F.A.G.: Albuquerque, P., Arrade, M., Arruda, M.,

Azevedo, M.O., Baptista, A.J., Bataus, L.A., Borges, C.L., Campos, E.G.,

Daher, B.S., Dantas, A., Ferreira, M.A.S., Gill, G.V.,

Nicola, A., Alves, E.S., Parente, J.A., Pereira, M.,

Nicola, A., Alves, E.S., Parente, J.A., Pereira, M.,

Nicola, A., Alves, E.S., Parente, J.A., Callal, G.V.,

Nicola, A., Alves, E.S., Parente, J.A., Callanha, R.R.,

Santos, S.C., Silva-Pereira, I., Silva, M.A.,

Santos, S.C., Silva-Pereira, I., Silva, M.A.,

Santos, S.C., Silva-Pereira, I., Silva, M.A.,

Andrade, E.V., Xavier, M.A.S., Veiga, H.P., Venancio, E.J.,

Andrade, E.V., Xavier, M.A.S., Veiga, H.P., Venancio, E.J.,

Andrade, E.V., Xavier, M.A., S., Veiga, H.P., Venancio, E.J.,

Carvalho, M.J.A., Oliveira, A.G., Inoue, M.K., Almeida, N.F.,

Walter, M. E.M.T., Soares, C.M.A. and Brighdo, M.M.

Transcriptome characterization of the dimorphic and pathogenic

fungus Paracoccidioides brasiliensis by EST analysis

Laboratory of Molecular Biology

Institute of Biology - University of Brasilia

Teal: SS 61 349 8411

Email: msuelianub, br.

Email: msuelianub, br.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:121759"
/clone lib="Mycelium and yeast cells from Paracoccidioides
brasiliensis"
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                                                                                                   EST 19-NOV-2002
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EST109-NOV-
EST000938 Mycelium and yeast cells from Paracoccidioides
brasiliensis Paracoccidioides brasiliensis CDNA, mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Pb Lambda Zap Express Library"
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Location/Qualifiers
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                                                                                                                                                                                           CA581263.1 GI:25129654
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Best Local Similarity
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Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetzaodon nigroviridis
Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis using Terracdon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.3%; Score 81.8; DB 29; Length 583; 44.7%; Pred. No. 2.9e-06; Live 46; Mismatches 125; Indels 1;
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/organism="Terracdon nigroviridis"
/mol_type="genomic DNA"
/db xref="taxon:99883"
/clone="082E19"
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nes 139; Conservative
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                                                                                                                                                                                                                                                   Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
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Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota, Metazca; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="Brain"
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CHORI-230 Rat (BN/SeNHsd/MCW) BAC library produced by
    Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
                                                                                                                                                                                                                                                                                                                                                       (http://www.chori.org/bacpac/orering_information.htm). BAC end page: http://www.tigr.org/tcdb/bac_ends/rat/bac_end_intro.html Plate: 120 row: K column: 23
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              Riggs.F., de-Dreggerigibs, b., Overton, b., Russell, D., Cr
Riggs.F., de-Grounders from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other GSSS: CH230-120K23.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 02200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'organism="Rattus norvegicus"
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|db_xref="taxon:10116"
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/cell type≈"B
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Web : www.genoscope.ons.fr)
This sequence is a single read and was generated as part of a large scale clone-descending project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.ons.fr/Tetraodon.
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Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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181C18 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="G"
/note="Genoscope sequence ID : COBGO82AC10SP1-end :
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Contact: Brendan J Loftus
Contact: Brendan J Loftus
Contact: Brendan J Loftus
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
Department of Eukaryotic Genomic Research
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 8208
Fax: 301 838 8243
Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microcorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas AgM Universty BAC Center
University. College Station, Texas 77843-2123, USA using a HindIII
Seq primer: M13 Por
Class: BAC ends.
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               GSS 10-DEC-2001
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Construction of a BAC library and generation of BAC end sequence-tagged connectors for genome sequencing of the African malaria mosquito Anopheles gambiae
Mol. Genet. Genomics 268 (6), 720-728 (2003)
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Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea,
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     S64 bp DNA linear GS:
AG-ND-119F15.TF ND-TAM Anopheles gambiae genomic clone
AG-ND-119F15, genomic survey sequence.
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/note="Vector: pECBAC1; Site_1: HindIII"
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/strain="PEST"
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/organism="Anopheles
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Matches 89,
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetracdon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.
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                      AL220040.1 GI:7878859
GSS; genome survey sequence.
Tetracdon nigroviridis
Tetracdon nigroviridis
Eukaryota, Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Nooteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes;
Tetracontoidea; Tetracodontidae; Tetracodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                       Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
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/note="Genoscope sequence ID : C0AG181BB09LP1~end : T7"
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                                                                                                                                                                                                                                                                                                           Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
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Doublished (2003)
Contact: Harris Lewin
Contact: Harris Lewin
Contact: Harris Lewin
Contact: Harris Lewin
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Contact: Harris Lewin
Contact: Harris Lewin
Contact: Harris Lewin
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
vailability, please contact Pieter de Jong (pdejong@mail.cho.org).
(http://www.chori.org/bacpac/ordering information.htm). This work
was underraken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by by University of Illinois at Urbana
Consortium (IBBMC) by by University of Illinois at Urbana
Champaign, USA with funds provided by grant No. Ag202-34480-11828
from USDA-CSREES and AG99-35205-8534 from USDA/NRI (Livestock
Genome Sequencing Initiative)
Plate: 130 row: L column: 13
Seq primer: T7
Class: BAC ends.
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Bovine BAC end sequences from CHORI-240 library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 12.1%; Score 80.4; DB 29; Length 602; Best Local Similarity 68.4%; Pred. No. 5.4e-06; Matches 108; Conservative 0; Mismatches 50; Indels 0
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/organism="Bos taurus"

/mol type="genomic DNA"

/strain="breed: Hereford"

/db_xref="taxon:9913"

/clone="CH240_130L13"
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Contact: Brendan J Loftus
Contact: Brendan J Loftus
Contact: Brendan J Loftus
Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@eligr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
F.H. Collins and sequenced by The Institute for Genomic Research
NNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from mirrorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M Universty BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 For
Class: BAC ends.
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CH240 130113.TV CHORI-240 Bos taurus genomic clone CH240_130113,
GC775881
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 602)
Larkin, D.M., Everts-van der Wind, A., Rebeiz, M., Schweitzer, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1— France 1 to 635)
Hong, Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J., Ren, C., Huff, E.R., Carlile, J.L., Black, K., Zhang, H.-B., Gardher, M.J. and Collins, F.H.
Construction of a BAC library and generation of BAC end sequence-tagged connectors for genome sequencing of the African malaria mosquito Anophales gambiae
Mol. Genet. Genomics 268 (6), 720-728 (2003)
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                  Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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/clone="%G-ND-180N8"
/clone=1ba="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
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/mol_type="genomic DNA"
/strain="PEST"
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Abv25006 Human CGD
Add782724 Human CGD
Add7844 Human CGD
Abx3548 Human CGD
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Abz75586 S
Abl29730 D
Abl10215 D
Acc85071 H
Aad57342 P
Aca56540 P
Acc85072 Aav20419 B
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-MODEL=frame+ p1. model -DEV=xlp
-MODEL=frame+ p2n. model -DEV=xlp
-Q=/cog1 _1/10SPTO spool p1.051078090/runat _20042004 _132809 _16579/app guery.fasta_1.455
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-DST TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XCAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DBLEXT=7
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Abx71178 Novel hum
Ab129731 Drosophil
Abx34636 Human mdd
Aax40058 Colon can
Aax40057 Colon can
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1 LRRAKAHEGLGFSIRGGSEH......TMANSAGGHSARSNLQTPG 260
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                3373863 segs, 2124099041 residues
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Listing first 45 summaries
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AAC75441
ADA53214
ABX71178
ABL29731
ABX34636
AAX40058
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Xgapop 10.0 , Ygapext (
Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext (
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1. geneseqn1980s:*

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The invention relates to human breast specific nucleic acids (I) comprising: (a) a sequence encoding any one of 95 protein sequences (ABP666708); (b) any one of 115 polymodeotide sequences (C ABP8356-ABP83672); (c) a molecule that selectively hybridizes to (a) or (b); (d) a molecule having at least 60% sequence identity to (a) or (b). (The breast specific nucleic acid molecules, polypeptides and antibodies or are useful for identifying, diagnosing, monitoring, staging, imaging and treating breast cancer and non-cancerous disease states in breast tissue. Or they are also useful for producing transgenic animals and cells and producing engineered breast tissue for treatment and research. The transgenic animals are useful as animal model systems used in elaborating the biological function of the polypeptides, studying conditions and/or disorders associated with aberrant expression and in screening for compounds effective in ameliorating the conditions. The polymucleotides
treating breast cancer and non-cancerous disease states in breast tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1677 BP; 407 A; 456 C; 473 G; 341 T; 0 U; 0 Other;
                                                             Claim 1; Page 171-172; 254pp; English.
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or Or	sequence 16// Br; 40/	4) 40p ()	0 11 150 15 515	o comer	
Alignme: Pred. M Score: Percent Best Lo Query M	nent Scores: No.: it Similarity: cocal Similarity: Match:	5.24e-106 1326.00 100.00% 100.00%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	1677 260 0 0	
US-10-	-078-090-151 (1-260)	x ABV83605	(1-1677)		
ζ	1 LeuArgArgAla	aLysAlaHisGl	GluGlyLeuGlyPheSer	IleArgGlyGlySerGluHis	20
QD	4 TIGCGGCGIGCC	AAGGCCCACGA	GGGCTTGGGCTTCAGC	TTGCGGCGTGCCAAGGCCCACGAGGCTTGGGCTTCAGCATCCGTGGGGGGCTTCGGAACAC	63
ò	21 GlyValGlyIle	TyrValSerLe	GlyValGlyIleTyrValSerLeuValGluProGlySerLeuAl	LeuAlaGluLysGluGlyLeu	40
Q	64 GGCGTGGGCATC	TACGTGTCTCT	GGTGGAACCAGGCTCT	GGCGTGGGCATCTACGTGTCTCTGGTGGAACCAGGCTCTCTAGCTGAGAAGGAAG	123
'n	41 ArgvalGlyAsi	ArgvalGlyAspGlnIleLeuArgValA	gValAsnAspLysSerL	LeuAlaArgValThrHisAla	09
QQ	124 CGGGTCGGGA	CAGATTCTGCG	CGTCAACGACAAATCC	CGGGTCGGGGGACCAGATTCTGCGCGTCAACGACAAATCCCTGGCCCGGGTGACCCAGGG	183
ò	61 GluAlaValLys	AlaLeuLysGl	aValLysAlaLeuLysGlySerLysLysLeuValLeuSerValTyrS	LeuSerValTyrSerAlaGly	80
Q	184 GAGGCCGTCAA	GCTCTGAAGGG	CTCCAAGAAGCTGGTG	GAGGCCGTCAAGGCTCCTGAAGGGCTCCAAGAAGCTGGTGCTGTCTGT	243
δ	81 ArgileProGly	GlyTyrValTh	rAsnHislleTyrTh	eProGlyGlyTyrValThrAsnHislleTyrThrTrpValAspProGlnGlyArg	100
q	244 CGCATCCCTGGGGG	GGCTACGTCAC	CAACCACATCTACACC	CTACGTCACCACACATCTACACCTGGGTGGACCCGCAGGGCCGC	303
È	101 SerlleSerProPr	ProSerGlyLe	uProGlnProHisGl)	VLeuproglnbroHisGlyGlyAlaLeuArgGlnGlnGlu	120
qa	304 AGCATCTCCC	ACCCTCGGGCCT	GCCCCAGCCCCACGG	GCATCTCCCACCCTCGGGCCTGCCCCAGCCCCACGGTGGTGCTCCTGAGGCAGCAGGAG	363
ò	121 GlyAspargar	SerThrLeuHi	GlyAspargArgSerThrLeuHisLeuLeuGlnGlyGlyAspGluLysLy	AspGluLysLysValAsnLeu	140
qq	364 GGTGACCGGAG	BAGCACCCTGCA	CCTCCTGCAAGGAGG	GGTGACCGGAGGAGCACCCTGCTCCTGCAAGGAGGGATGAGAAAAAGGTGAAACCTG	423
δ,	141 ValLeuGlyAs	oglyArgSerLe	uGlyLeuThrileArg	ValleuGlyAspGlyArgSerLeuGlyLeuThrIleArgGlyGlyAlaGluTyrGlyLeu	160
qq	424 GTGCTGGGGA	GGCCGGTCCCT	regecercacaarecer	GTGCTGGGGGACGGCCGGGTCCCTGGGCTCACGATCCGTGGGGGGGG	483
ò	161 GlylleTyrll	eThrGlyValAs	GlylleTyrlleThrGlyValAspProGlySerGluAlaGluGlySerGlyL	GluGlySerGlyLeuLysVal	180
qa	484 GGCATTTACATCACTGG	CACTGGCGTGGA	ACCCAGGCTCTGAAGC	cccaeectcteaaecaeaadecaececccaaectr	543
ò	181 GlyAspGlnIl	GlyAspGln1leLeuGluValAsnGlyArgSer	snGlyArgSerPheLe	PheLeuAsnIleLeuHisAspGluAla	200
QQ	544 GGGGACCAGAT	-⊢	ATGGGGGGGGCTTTCT	chagaagtgaardgacdgagcrrrchagaacdacgacgacg	603
8,	201 ValArgLeuLe	uLysSerSerAı	rgHisLeulleLeuTh	ValArgLeuLeuLysSerSerArgHisLeuIleLeuThrValLysAspValGlyArgLeu	220

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AAC7446 to AAC77606 encode the proteins given in ABB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipactiatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiparkinsonian; nootropic; antidiabetic; hypotensive; deradiant; thrombolytic; coagulant; vsottopic; antidiabetic; hypotensive; antiviral; immunosuppressive; antiniflammatory; antibacterial; antiviral; antifungal; antirheumatic; antihinflammatory; antibacterial; acquences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX
604 GTCAGGCTGCTTAAGTCATCTCGGCACCTCATCCTGACAGTGAAGGACGTCGGGAGGCTG 663
                                                                    240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; vulnerary; antipsoriatic; antiarthritic; immunosupessant; cardiant; immunosupessant; cardiant; immunosupensive; dermatological; immunosuperssive; antidiabetic; hypotensive; dermatological; immunosuperssive; antidiamatory; antianeamic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; beneficiency; and antidiammatory disease; coagulation;
                                                                                                                                                                                                724 Accardeceaacrceecaedearcreeccacrerecreercaarcreeaececaege
                                                                                           664 CCCCATGCCCGCACCACTGTGGACGAGACCAAGTGGATCGCCAGTTCCCCGGATCAGGGAG
                                                                                                                                                        241 ThrMetAlaAsnSerAlaGlySerGlyHisSerAlaArgSerAsnLeuGlnThrProGly
                                                                    ProHisAlaArgThrThrValAspGluThrLysTrpIleAlaSerSerArgIleArgGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                      Human ORFX ORF996 polynucleotide sequence SEQ ID NO:1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 1517-1519; 5507pp; English
                                                                                                                                                                                                                                                                                          AAC75441 standard; cDNA; 3102 BP.
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02-APR-1999; 99US-0127636P.
05-APR-1999; 99US-0127728P.
30-MAR-2000; 2000US-00540763.
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P-PSDB; AAB41232.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             854
proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                             gserIleSerProProSerGlyLeuProGlnProHisGlyGlyAlaLeuArgGlnGlnGl 120
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                                                                                                          Other;
                                                                                                         Sequence 3102 BP; 699 A; 996 C; 860 G; 545 T; 0 U; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynuclectides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases which the gene is involved, or as target molecules for gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel human secretory or membrane proteins (ADAS4072-ADAS5710) and their coding sequences (ADAS4041). The coding sequences are useful in the gene therapy of diseases caused by abormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
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(REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                           Human coding sequence, SEQ ID
                                                                                                                           ADA53214 standard; cDNA; 1718
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24-JAN-2002; 2002US-0350435P.
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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CGGGTCGGGGACCAGATTCTGCGCGTCAACGACAAATCCCTGGCCCGGGTGACCCACGCG 1255
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                                                                                                                                           GAGGCCGTCAAGGCTCTGAAGGCTCCAAGAAGCTGGTGTGTCTGTGTACTCAGCAGGG
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Drmanac RT;
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I, Wang
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Wehrman T,
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lateral sclerosis); neurodegenerative diseases (e.g. Parkinson's disease, Alzheimer's disease); autoimmune disease (e.g. systemic lupus erythematosus, rheumatoid arthritis, insulin-dependent diabetes mellitus); myeloid or lymphoid cell disorders (e.g. ansemia and thrombocytopaenia); myeloid or lymphoid cell disorders (e.g. osteoporosis, costeomical lateral and traumatic disorders (e.g. stroke, head traumal); lung or liver fibrosis; reperfusion injury in various tissues; bacterial, viral or fungal infections; allergic conditions such as cancer and tumours; and inflammatory diseases (e.g. septic shock, Crohn's cancer and tumours; and inflammatory diseases (e.g. septic shock, Crohn's care and tumours; and inflammatory diseases (e.g. septic shock, Crohn's confection of function may be used to inhibit the growth, viruses, or to effect bodily characteristics, biorhythms or circadian cycles of rhythms. The protein may also have for a soceria, fungi, viruses, or to effect bodily characteristics, biorhythms or circadian cycles of rhythms. The protein may also have function, differentiation, stem cell growth factor, haematopoiesis; regulation, immune stimulating or suppressing, chemotactic/chemokinetic, hemostatic and thrombolytic, receptor/ligand, and antiinflammatory activities. The cDNA sequences of the invention are useful for expressing recombinant protein for analysis. The present sequence is an expressed human cDNA sequence of the invention, this sequence is an expression cardument protein defined invention, this sequence is an expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MDDI, human, disease detection and treatment molecule polypeptide; anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV; demenostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic; gene therapy; protein replacement therapy; cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma; anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS; Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia; psoriasis; hepatitis; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                   114 GlyAlaLeuArgGlnGlnGluGlyAspArgArgSerThrLeuHisLeuLeuGlnGlyGly 133
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                                    20 HisGlyValGly------IleTyrValSerLeuValGluProGlySer
                                                                                                                34 LeuAlaGluLysGluGlyLeuArgValGlyAspGlnIleLeuArgValAsnAspLysSer
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                                                             46 CACGGCTTCGGTCCCCCCCCCGCGACCCCATGTACGCATCGATGGATCCCCCC-------
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                                                                                                                                                                                         987 GACCGACTGAGCAACGGGGTGCTGCAGCAGTGTCCCCGGCCTCTGAGAGCAGCTCCAGC 1046
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                                                                              214 VallysAspValGlyArgLeuProHisAlaArgThrThrValAspGluThrLysTrpIle 233
                                                                                                                                                           -----AlaSerSerArgIleArgGluThrMetAlaAsnSerAlaGlySerGlyHisSer 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                       AsnileLeuHisAspGluAlaValArgLeuLysSerSerArgHisLeuIleLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
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11-JUL-2000; 2000US-00614150.
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1015 GGCAGCGTGAGCT-GCAGCGGCAGGAGCTTCTCATGCAGAAGCGGCTGGCGATGGAGTC 1073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335 GAGGAGGTCATCAACCTCATTCGAACCAAGAAACTGTGTCCATCAAAGTGAGACACATC 594
                                                                                                                                                                                                               98 GlnGlyArgSerIleSerProProSerGlyLeuProGlnProHisGlyGlyAlaLeuArg 117
                                                                                                                                                                                                                                                                                                  118 GlnGlnGluGlyAspArgArgSerThrLeuHisLeuLeuGlnGlyGlyAspGluLysLys 137
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475 CTCCAGGTAGGGGACGAGATCGTCCGGATCAATGGATATTCCATCTCCTCTGTACCCAT 534
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breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
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                                         60 AlaGluAlaValLysAlaLeuLysGlySerLysLysLeuValLeuSerValTyrSerAla
                                                                                                                                                                    158 TyrGlyLeuGlyIleTyrIleThrGlyValAspProGlySerGluAlaGluGlySerGly
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                                                                                                                             80 GlyArgileProGlyGlyTyrValThrAsnHisIleTyrThrTrp-----ValAspPro
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97US-0061599P.
97US-0061765P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel disease detection and treatment molecule polypeptide (MDDT) which has anti-inflammatory, immunosuppressive, osteopathic, vytostatic, anti-HIV, haemostatic, nephrotropic ontianaemic, attipsoriatic and hepatotropic activity. The polymunosuppressive, conditions antianaemic activity. The polymunosuppressive, conditions of the invention can be used for gene therapy, conditions. These polypeptides or polymunostides are particularly useful for diagnosing, treating a variety of particularly useful for diagnosing, treating or preventing call particularly useful for diagnosing, treating or preventing call conditions, melanoma, melanoma, melanoma, mayeloma or sarcoma, anaemia, Crohn's disease, acquired immunodeficiency syndrome (MIDS), doodpasture's conditions, inflammation, osteoporosis, thombocytopaenia, psoriasis or hepatitis. ABX3440-ABX34835 encode the MDDT polypeptides represented in ABCHISO-MULI9845, described in the disclosure of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New purified disease detection and treatment molecule proteins and polynucleotides, useful for diagnosing; treating or preventing cancers (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis or hepatitis.
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                                                                                                                                                                                                                                                                                                                                                                 Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2259 BP; 555 A; 598 C; 661 G; 445 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 197; 339pp + Sequence Listing; English.
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29-MAR-2001; 2001US-0280067F.
16-MAY-2001; 2001US-029180F.
17-MAY-2001; 2001US-0291829F.
17-MAY-2001; 2001US-0291849F.
19-UUN-2001; 2001US-029948F.
20-UUN-2001; 2001US-0299776F.
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51.88%
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P-PSDB; ABU11646.
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Best Local Similarity:
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Query Match:

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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigaen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product with an agent that specifically product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions that invention provides nucleic and sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                             polypeptides - isolated products for the
                                                                              Stockert E, Gure A, Chen Y, Gout I; Pfreundschuh M, Tureci O, Sahin U;
                                                                                                                                                                           New isolated cancer associated nucleic acids and using sera from cancer patients, used to develop diagnosis, monitoring or treatment of cancers.
                                                                                                                                                                                                                                                                Claim 67; Page 658; 787pp; English
                                       (LUDW-) LUDWIG INST CANCER RES
98US-00102322
                                                                              Scanlan MJ,
Obata Y,
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  22-JUN-1998;
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2162 BP: 528 A: 573 C: 622 G: 439 T: 0 U: 0 Other

2162 BP; 528 A; 573 C; 622 G; 439 T; 0 U; 0 Other;	res: 4.1e-18 Length: 2162 318.50 Marches: 93 1rity: 51.88* Conservative: 45 nilarity: 34.02* Indels: 27 24.02* Gaps: 8	.151 (1-260) x AAX40058 (1-2162)	LeuargargalaLysalaHisGluGlyLeuGlyPheSerIleArgGlyGlySerGlu 19	GIGCGICTGGACCGTCTGCACCCCCGAAGGCCTCGGCCTGAGTGTGCGTGGGTGCCTTGGAG 417	HisGlyvalGlyIleTyrValSerLeuValGluProGlySerLeuAlaGluLysGluGly 39	TTTGGCTGTGGGCTCTTCATCTCCCACCTCAAAGGCGGTCAGGCAGACAGCGTCGGG 477	2,7	CICCAGGIAGGGGAC	AlaGluAlaValLysAlaLeuLysGlySerLysLysLysLeuValLeuSerValTyrSerAla 79	GAGGAGGTCATCAATCGAACCAAGAAACTGTGTCCATCAAAGTGAGACACATC 597	GlyargileProGlyGlyTyrValThrAsnHislleTyrThrTrpValAspPro 97		GlnGlyArgSerIleSerProProSerGlyLeuProGlnProHisGlyGlyAlaLeuArg 117	CAGTTTGTGTCGGGATCTGGGGGCGTGCGAGGCAGCCTGGGC 696	GlnGlnGluGlyAspArgArgSerThrLeuHisLeuLeuGlnGlyGlyAspGluLySLys 137	TCCCCTGGAAATCGGGAAAACAAGGAAGAAAAG 729	ValAsnLeuValLeuGlyAspGlyArgSerLeuGlyLeuThrIleArgGlyGlyAlaGlu 157	GICTICATCAGCCTGGTAGGCTCCCGGAGGCTTGGCTGCAGCATTTCCAGCGGCCCCATC 789
2162	Scores: milarity: Similari h:	-151	1 LeuArgA	358 GIGCGIC	20 Hisglyva	418 TTTGGCT	40 LeuArgV	478 CTCCAGG	60 AlagluA	538 GAGGAGG	80 GlyArgi	598 GGCCTGA	98 GlnGlyA	- 1	118 GlnGlnG	697TCCC	138 ValAsnL	730 GTCTTCA
SQ Sequence	Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	US-10-078-090	à	QQ	λ	QQ	٥٧	Db	ζ	QC	ò	qq	ò	Dp	à	qq	λō	Dþ

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the
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breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
prostate cancer; ss.
158 TyrGlyLeuGlyIleTyrileThrGlyValAspProGlySerGluAlaGluGlySerGly
                   CAGAAGCCTGGCATCTTTATCAGCCATGTGAAACCTGGCTCCCTGTCTGCTGAGGTGGGA
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10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
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interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and lung cancer

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Sequence 2236 BP; 548 A; 588 C; 653 G; 447 T; 0 U; 0 Other;

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ACATC 597

CCCAT 537

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hrHis 59

TCGGG 477

luGly 39

TGGAG 417

erglu 19

3ÀT--- 654 euArg 117 969 -----

sspPro 97

CCATC 789 SerGly 177 STGGGA 849 LeuHis 197 GATCAC 909

MaGlu 157

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    isolated the

                                                                                                                 Cancer associated antigen; diagnosis; research; treatment; human;
breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                    New isolated cancer associated nucleic acids and polypeptides using sera from cancer patients, used to develop products for diagnosis, monitoring or treatment of cancers.
                                                                                                                                                                                                                                                                                                           Gout I;
in U;
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Pfreundschuh M, Tureci O, Sahin
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                1077 CAACAAGATCCTCCAGGA 1094
                                                  ВР
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97US-0061599P.
97US-0061765P.
97US-0094870S.
97GB-00021697.
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                                                  AAX39644 standard; DNA; 2236
                                                                                                       Renal cancer associated gene.
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Gln-----ThrProGly
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10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
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257
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Sequence 2236 BP; 548 A; 588 C; 653 G; 447 T; 0 U; 0 Other; lung

The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contexting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination between the agent and the NAM or the expression product as a chetermination for the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, gastric cancer, prostate cancer and

Alignment Scores:			
	ď	Length:	2236
Score		Matches:	93
Percent Similarity:	1.88%	Conservative:	45
al Simi	4.96%	Mismatches:	102
tch:	4.02	Indels:	27
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GAGGCG 1017

SerSer 236

LysAsp 216

GCTGCA 969

GGAGTC 1076 256

AsnLeu

US-10-078-090-151 (1-260) x AAX39644 (1-2236)

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970 GCTGGCCGG------GAGCTGTTCATGACAGACCGGAGCGCCTGGCAGAGGCG 1017
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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigon precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically biological sample isolated from a subject with an agent that specifically brinds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, remal cancer, colon cancer, gastric cancer, prostate cancer and
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97US-0061599P.
97US-0061765P.
97US-00948705.
97GB-00021697.
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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a mucleic acid molecule (TAMM). The method comprises: (a) contexting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions of pharacterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast and cancer, colon cancer, gastric cancer, prostate cancer and
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97US-00948705.
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                                                                                                                                                                           ArgileArgGluThrMetAlaAsnSerAlaGlySerGlyHisSerAlaArgSerAsnLeu 256
                                                            ValGlyArgLeuProHisAlaArgThrThrValAspGluThrLysTrpIleAlaSerSer 236
      910 AAGGAGGCTGTAAATGTGCTGAAAATAGCCGCAGCCTGACCATCTCCATTGTAGCTGCA 969
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05-FEB-2002; 2002EP-00290277.
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P-PSDB; ABP71383.
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                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticidaes, therapeuticing and pharmaceutical frugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-BPINGOR). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 LeuHisAspGluAlaValArgLeuLeuLysSerSerArgHisLeuIleLeuThrValLys 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspValGlyArgLeuProHisAlaArgThrThrValAspGluThrLysTrpIleAlaSer 235
                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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                                                                                                                                                  Claim 1; SEQ ID NO 40663; 21pp + Sequence Listing; English.
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                                 (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1489 BP; 323 A; 398 C; 485 G; 283 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 25127; 21pp + Sequence Listing; English
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                                                   Drosophila melanogaster
pharmaceutical; gene;
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P-PSDB; ABB66112.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying a candidate beta-catenin pathway modulating agent for diagnosing or treating cancer by detecting a test agent-blased activity of the assay system comprising a purified MBCAT polypeptide or nucleic acid.
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|-----GTIGCGAGCCGCGACATCAGTGTGGTCCTCCATGTGGCGCCCAGGACGAAGCTG
GlnGlyGlyAspGluLysLysValAsnLeuValLeu-----GlyAspGlyArgSerLeu
                                                                                                           GlyLeuThrileArgGlyGlyAlaGluTyrGlyLeuGlyIleTyrIleThrGlyValAsp
                                                                                                                                               169 ProGlySerGluAlaGluGlySerGlyLeuLysValGlyAspGlnIleLeuGluValAsn
                                                                                                                                                                                                                                                           GATCGGAGTGTCGCCCGGGAGGCGGGATTACGGCCAGGTGACCAGATCCTCAGCGTCAAC
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13-DEC-2001; 2001US-0340314P.
13-DEC-2001; 2001US-0340322P.
15-PEB-2002; 2002US-035502P.
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Mismatches:
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Sequence 48, Application US/10078090

Sequence 48, Application US/10078090

Publication No. US20000044815A1

GENERAL INFORMATION:

APPLICANT: Macina, Roberto

APPLICANT: Rarra, Kalpana

APPLICANT: Rarra, Kalpana

APPLICANT: Cafferkey, Robert

APPLICANT: Cafferkey, Robert

APPLICANT: Cafferkey, Robert

APPLICANT: Cafferkey, Robert

APPLICANT: Cafferkey, Robert

APPLICANT: Cafferkey, Robert

APPLICANT: Liu, Chenghua

TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and P)

TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and P)

CURRENT FILING DATE: DEX-0310

CURRENT FILING DATE: 2001-02-14

PRIOR APPLICATION NUMBER: 60/268,999

PRIOR APPLICATION NUMBER: 60/268,999

PRIOR APPLICATION UNESE: 210

CURRENT FILING DATE: 2001-02-15

NUMBER OF SEQ ID NOS: 210

SOFTWARE PATENTIAL VERSION 3.1

SEQ ID NO 48

LENGTH: 1677
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13 US-10-112-984-536
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-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/Cogn_1/USFTO spool p/US10078090/runat_20042004_132811_16613/app_query.fasta_1.455
-DS=Published Applications NA -QFNT=fastap -SUFFIX=p2n.rnpb -MINNATCH=0.1
-LOOPCI=0 -LOŌPEXT=0 -UNITS=bits -STRAT=1 -END=-1 -WATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFNT=Ptc -NORM=ext -HBARSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=US10078090 @CGN 1 1333 @runat 20042004 132811_16613
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TINEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDF=10 -XGAPEXT=0.5
-FGAPOP=6 -FGĀPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1326
1 IRRAKAHEGLGFSIRGGSEH.....TMANSAGSGHSARSNLQTPG 260
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
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        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                2.74e-145
1326.00
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; TYPE: DNA
; ORGANISM: Homo sapien
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                                         Alignment Scores:
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GlyaspGlyargSerLeuGlyLeuThrIleArgGlyGlyAlaGluTyrGlyLeuGlyIle 162
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20 GGCCCACGACTACTTCCTCCTGAGTGCCGTTCAGTGGCC-------TGT
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APPLICANT: Zhang, Jie
APPLICANT: Red, Addong J.
APPLICANT: Red, Addong J.
APPLICANT: Red, Addong J.
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: When Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Coing A.
APPLICANT: Wang, Zhiwei
ITILE OF INVENTION: Secreted Polypeptides
FILE REFERENCE: 805A
CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT FILING DATE: 2000-01-21
PRIOR PILING DATE: 2000-01-21
PRIOR PILING DATE: 2000-02-03
PRIOR PILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR PILING DATE: 2000-02-28
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ORGANISM: Homo sapiens
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Best Local Similarity:
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                                                                                           1196 CGGGTCGGGGACCAGATTCTGCGCGTCACAAAATCCCTGGCCCGGGTGACCCAGGG
                                                                                                                                                                                  81 ArgileProGlyGlyTyrValThrAsnHisIleTyrThrTrpValAspProGlnGlyArg
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                                                                       41 ArgvalGlyAspGlnIleLeuArgValAsnAspLysSerLeuAlaArgValThrHisAla
                                                                                                                                                 61 GluAlaValLysAlaLeuLysGlySerLysLysLeuValLeuSerValTyrSerAlaGly
GlyvalGly1leTyrvalSerLeuValGluProGlySerLeuAlaGluLysGluGlyLeu
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APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Nang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
TITLE OF INVENTION: No. US20030219745A1e1 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802COM
CURRENT APPLICATION NUMBER: US/10/120,988
CURRENT APPLICATION NUMBER: 09/774,528
FRIOR APPLICATION NUMBER: 09/774,528
FRIOR APPLICATION NUMBER: 09/774,528
NUMBER OF SEQ ID NOS: 441
SEQ ID NOS: 441
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438.00
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ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: (66)..(2822)
US-10-120-988-406
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Best Local Similarity:
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US-10-120-988-406
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                                                                                                                                                                                  482 CIGCIIAAGICAICTCGGCACCTCAICCTGACAGIGAAGGACGTCGGGAGGCTGCCCCAI 541
                                                                                                                                                                                                                              223 AlaArgThrThrValAspGluThrLysTrpIleAlaSerSerArgIleArgGluThrMet 242
                                           421
                                                                                                                                                                                                                                                542 GCCGCACCACTGTGGACGAGACCAAGTGGATCGCCAGTTCCCGGATCAGGGAGCCATG 601
                                                                                                                                                                                                                                                                                                    243 AlaAsnSerAlaGly---SerGlyHisSerAlaArgSerAsnLeuGlnThrProGly 260
                                                                                                                                                                                                                                                                                                                                         602 gegaacregecaggerretregegarereaeaagaagaaraaacaagcaaga 658
       TyrileThrGlyValAspProGlySerGluAlaGluGlySerGlyLeuLysValGlyAsp
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Mismatches:
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GENERAL INFORMATION:
APPLICANT: SUGIXAMA, TOMOYASU
APPLICANT: SUGIXAMA, TOMOYASU
APPLICANT: SUGIXI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISANO, YUUKO
APPLICANT: ISONO, YUUKO
APPLICANT: HORAL, KEICHI
APPLICANT: NAGAI, KEICHI
APPLICANT: NAGAI, KEICHI
APPLICANT: SEKI, NACHIKA
APPLICANT: RASUIKA
APPLICANT: SEKI, NACHIKA
APPLICANT: SEKI, NACHIKA
APPLICANT: SEKI, NACHIKA
APPLICANT: SOFIKAMA, TSUTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGHARI, KENJI
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APPLICANT: NAGHARI, KENJI
APPLICANT: NAGHARI: 2010-094,749
CURRENT FILING DATE: 2001-0328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 78:
LENGTH: 1718
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Matches:
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; ORGANISM: Homo sapiens
US-10-094-749-782
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Best Local Similarity:
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US-10-094-749-782
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Sequence 17426, Application US/20030194704A1

GENERAL INFORMATION:
APPLICANT: Fear, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPOSITE 2001-112-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 17428
LINNGTH: 195
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PEATURE: DOTHER INFORMATION: MAP TO AL138895.4 SIGNAL = 0.63
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.63
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.63
OTHER INFORMATION: BY HIT: BE890168.1, EVALUE 1.00e-105
OTHER INFORMATION: WI HIT: 9114735271, EVALUE 1.00e-106
US-10-029-386-17428
BF969269.1, EVALUE 0.00e+00
P54817, EVALUE 3.70e-02
                                                                                                                                                                                                                                         34 AAATCGAGGGCTAGAAAGGAAAGGGA-----CTTCAGGGCTGG----
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Mismatches:
Indels:
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Matches:
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SWISSPROT HIT:
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Best Local Similarity:
   ; OTHER INFORMATION:
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US-10-029-386-3728
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US-10-029-386-17428
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                                                                 504 GGTAGCGCCGTAAAGGTGCTGACCAGCAGCCGCCTGCACATGATGGTTCGGCGCATG 563
        CATGGCCTGGGCATCTTCGTCAGCAAAGTGGAAGGAAGGCAGCAGTGCAGAGCGGGCTGGC 443
                                                                                              60 AlaGluAjayajiyaAlaLeuLysGlySerLysLysLeuValLeuSerVajTyrSerAla 79
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                                    LeuargvalGlyaspGlnileLeuargvalaspaspLysSerLeualaargvalThrHis 59
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OTHER INFORMATION: MAP TO AL138895.4
OTHER INFORMATION: EXPRESED IN HELA, SIGNAL = 0.63
OTHER INFORMATION: NT HIT: g114735271, EVALUE 1.00e-123
                                                                                                                                                                                                                                         1047 GTCTCTTCG 1055
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ORGANISM: Homo sapiens
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US-10-029-386-3728
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Page 5

Alignment Scores: Pred. No.: Score: Score: 146.00 Marches: 65 Bert Local Similarity: 100.00% Mismatches: 0 Query Match: 15.09% Indels: 0 Gaps: 0	87 25 10 30
US-10-078-090-151 (1-260) x US-10-029-386-17428 (1-195)  QY 65 AlaLeulysGlySerLysLeuValLeuSerValTyrSerAlaGlyArglleProGly 84  Dh	Qy 106 SerGlyLeuProGlnProHisGlyGlyAlaLeuArgGlnGluGlyAspArgArgSer 125
85 61	Db 355AAGGAGAAGAAGAAGATTTATCHACGGGCTCT 390 Oy 146 ArgSerLeuGlyLeuThrileArgGlyGlyAlaGluTyrGlyLeuGlyLeuGhrileThr 165
Oy 105 ProSerGlyLeuProGlnProHisGlyGlyAlaLeuArgGlnGlnGluGlyAspArgArg 124	
Oy 125 SerThrLeuHisLeu 129  Db 181 AGCACCTGCACTC 195	Db 451 CACGTGAAGCCTGGCTCCCTGTCTGCAGAGGGGGTTAGAGACAGGAGACCAGATTGTG 510  Qy 186 GluvalAenGlyArgSerPheleuAsnIleLeuHisAspGluAlaValArgLeuLeuLys 205
	206
	Oy 216 AspValGlyArgLeuProHisAlaArg 224
; APPLICANT: Boeda B. ; APPLICANT: EL-Amraoui A. ; TITLE OF INVENTION: More Protein-Protein Interactions In The Inner Ear ; FILE REFERENCE: BANDABER: US/10/177.191A	RESULT 8 US-10-305-720-1138 ; Sequence 1138, Application US/10305720 ; Publication No. US20040010136A1
	; GENERAL INFORMATION: ; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J. ; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressic; FILE REPERENCE: PA-0002-1 CON ; CURRENT APPLICATION NUMBER: US/10/305,720
37 Human A-5	CURRENT FILING DATE: 2002-11-26  PRIOR APPLICATION NUMBER: 09/016,434  PRIOR FILING DATE: 1998-01-30  NUMBER OF SEQ ID NOS: 1490  SOFTWARE: PERL PROGRAM
Alignment Scores: 8.07e-27 Length: 837  Pred. No.: 312.00 Matches: 83  Score: 31.53 Conservative: 35  Best Local Similarity: 36.24\$ Mismatches: 83  Query Match: 15.53\$ Gaps: 6  DB:	) SMUCH: 3071 ) TYPE: DNA ) CRGANISM: Homo sapiens ) PEATURE: misc feature ) OTHER INFORMATION: Genbank ID No. US20040010136A1 g1463025 US-10-305-720-1138
US-10-078-090-151 (1-260) x US-10-177-191A-5 (1-837)  QY	Alignment Scores: 2.55e-16 Length: 3071 Score: 229.00 Matches: 104 Percent Similarity: 39.83% Conservative: 38 Best Local Similarity: 17.73% Mismatches: 90
Qy 28 LeuValGluProGlySerLeuAlaGluLySGluGlyLeuArgValGlyAspGlnIleLeu 47 :::	16 Gaps: 1-260) x US-10-305-720-1138 (1-3071
Qy 48 ArgvalAsnAspLysSerLeuAlaArgValThrHisAlaGluAlaValLysAlaLeuLys 67	Qy 5 LysalaHisGluGlyLeuGlyPheSerIleArgGlyGlySerGluHisGlyVal 22

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                                                                                                                                                                               1138 TATGGTCCACCTGATATTACTCACTCTTATTCTCCACCAAGGAAAACCATCTACTCTCT 1197
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                                                                                                                                  .048 cacgaagaggcagtaggcaataftaaagaacacatcagaggtagttartttaaaagttggc 1107
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                                                                              988 AGGTTGCAAGTAGGAGATAGACTACTAATGGTAAACAACTACAGTTTAGAAGAAGTAACA 1047
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               HisAlaGluAlaValLysAlaLeuLysGlySerLysLysLeuVal ---LeuSerValTyr 77
                                                                                                                                                            78 SerAlaGlyArgileProGlyGlyTyrValThrAsnHisIleTyrThrTrpValAspPro 97
Gly------ileTyrvalSerLeuValGluProGlySerLeuAlaGluLysGluGly 39
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US-10-451-207-14
Sequence 14, Application US/10451207
Publication No. US20040038267A1
GENERAL INFORMATION:
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; OTHER INFORMATION: Incyte ID No. US20040038267A1 6942051CB1
US-10-451-207-14
                                                                                                                                                                                                                                                                                      APPLICANT: FARMS, Y. TOM
APPLICANT: KHAN, Y. TOM
APPLICANT: KHAN, Y. TOM
APPLICANT: KHAN, Y. TOM
APPLICANT: KHAN, Y. TOM
APPLICANT: KHAN, PEATEN A.
APPLICANT: EMERING, Brooke M.
TITLE OF INVENTIONS: INTRACELLULAR SIGNALING MOLECULES
FILE REPERENCE: PF-0688 USN
CURRENT APPLICATION NUMBER: US/10/451,207
CURRENT APPLICATION NUMBER: US/10/50315
PRIOR APPLICATION NUMBER: PCT/US01/50315
PRIOR APPLICATION NUMBER: US 60/257,804
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: US 60/260,102
PRIOR APPLICATION NUMBER: US 60/260,102
PRIOR PILING DATE: 2000-12-21
PRIOR PILING DATE: 2000-12-21
PRIOR PILING DATE: 2000-12-21
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NUMBER OF SERL PROGRAM
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                     VUE, Henry
THORNTON, Michael B.
CHAMLA, Narinder K.
GANDHI, Ameena R.
ARVIZU, Chandra S.
BAUGHN, Mariah R.
SWARNAKAR, Antea
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THANGAVELU, Kavitha
WARREN, Bridget A.
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BURFORD, Neil
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LENGTH: 5139
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gg		Db 1649 GAGGACGTCATGCAT
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3 8	Σ	Db 1985 GGTGAAGGCATCTTV Ov 178 LeuLysValGlyAsg
qq	3631 TITGCGGCAGGCATCGGCCACCGGAACAGCCTGGAGAGC 3669	2045
RESULT US-09-9 ; Seque ; Pater	RESULT 10 US-09-919-497-9 ; Sequence 9, Application US/09919497 ; Patent No. US2002106662A1 ; GENERAL INFORMATION:	8
, APP]	ICANT: Mutter, George L. B OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER	0 10
FILE	REFERENCE: B0801/7225 ENT APPLICATION NUMBER: US/09/919,497	UD ZIES MANCAGANGIA Z38 IleAraGluThrMe
, COR	ENT FILING DATE: 2001-07-31 SR APPLICATION NUMBER: US 60/221,735	2207
NUM; SOF	SOFTWARE: Patentin version 3.0	RESULT 11 US-10-170-385-300 ; Sequence 300, Application
; LENGT ; TYPE: ; ORGAN US-09-919	LENGTH: 3995 LYPE: DNA ORGANISM: Homo sapiens 9-919-497-9	; Publication No. Ug20030203 ; GENERAL INFORMATION: ; APPLICANT: Ward, Neil Ray ; APPLICANT: Mindy, Christ
Alignm Pred. Score: Percen Best L Query DB:	Alignment Scores: 2.42e-15 Length: 3995 Score: 222.00 Matches: 91 Score: Percent Similarity: 46.45\$ Conservative: 40 Best Local Similarity: 32.27\$ Mismatches: 110 Query Match: 9 Gaps: 13	APPLICANT: Kan, On APPLICANT: Haris, Rober APPLICANT: White, Jonath APPLICANT: While, APPLICANT: Rayner, Willi APPLICANT: Rayner, Willi APPLICANT: Kries. Bania , APPLICANT: Kries. Bania , APPLICANT: Kries. Bania
US-10-	US-10-078-090-151 (1-260) x US-09-919-497-9 (1-3995)	; TITLE OF INVENTION: ANALY FILE REFERENCE: 532682000
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çy d	19 GluHisGlyValGlylleTyrValSerLeuValGluProGlySerLeuAla 35	, PRIOR APPLICATION NUMBER: , PRIOR FILING DATE: 2001-1, , NUMBER OF SEQ ID NOS: 549 , SOFTWARE: FASTSEO for With
ે દ	36 GluLysGluGlyLeuArgValGlyAspGlnIleLeuArgValAsnAspLysSerLeu 54	; SEQ ID NO 300 ; LENGTH: 3995 ; TYPE: DNA
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yrileThrGlyValAspProGlySerGluAlaGluGlySerGly--- 177
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TCATCTCCTTIATCCTGGCGGGGCCTGCAGACCTCAGTGGGGAG 2044
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                                                   Score:
Percent Similarity:
Best Local Similarity:
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US-10-276-774-724/c
ORGANISM: Homo
  ; OKGANISM: ACM
US-10-170-385-300
                             Alignment Scores:
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Sequence 724, Application US/10276774; Publication No. US20040053245A1

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3125 ACACCAAGGACCAAAATGTTCACGCCTCCATCAGAGTCTCAGCTGGTGGACACGGGAACC 3066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------ProSerGlyLeuProGlnProHisGlyGlyAlaLeuArgGlnGlnGlu 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---GlyAspArgArgSerThrLeuHisLeuLeuGlnGlyGlyAspGluLysLysValAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgvaldlyAspClnIleLeuArgvalAsnAspLysSerLeuAlaArgvalThrHisAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluGlySerGly---LeuLysValGlyAspGlnIleLeuGluValAsnGlyArgSerPhe
                                  Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --SerGluHisGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 ValGlyIleTyrValSer -- - LeuValGluProGlySerLeuAlaGluLysGluGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlualavallysalaleulysGlySerlysLys------
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APPLICANT: Hyaeq, Inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: No. US20040053245Alel Nucleic Acids and Poly,
TITLE OF INVENTION: No. US20040053245Alel Nucleic Acids and Poly,
FILE REFERENCE: 2122-030
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR APPLICATION NUMBER: 09/496,914
NUMBER OF SEQ ID NOS: 2700
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848
8444
2444
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Mismatches:
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Matches:
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203.00
46,42%
28.30%
15.31%
                                                                                                                                                                                                                                                         , ORGANISM: Homo sapiens
US-10-276-774-724
                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                        SEQ ID NO 724
LENGTH: 4235
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APPLICANT: SILexan, Karen
APPLICANT: Glories M.
APPLICANT: Grosse, William M.
APPLICANT: Alsobrock II, John P.
APPLICANT: Alsobrock II, John P.
APPLICANT: Alsobrock II, John P.
APPLICANT: Padigaru, Muralidhara
APPLICANT: Banesh
APPLICANT: Banesh
APPLICANT: Banesh
APPLICANT: Banesh
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Slinkets, Bichard A.
APPLICANT: Slinkets, Bichard A.
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APPLICANT: Slinkets, Bichard A.
APPLICANT: Slinkets, Bichard A.
APPLICANT: Slinkets, Bichard A.
APPLICANT: Slinkets, Gold-09-27
APING PILING DATE: 2000-09-27
APING PILING DATE: 2000-09-27
APING APPLICATION NUMBER: GOld-36,065
APING APPLICATION NUMBER: GOld-38,321
APING APPLICATION NUMBER: GOld-38,321
APING APPLICATION NUMBER: GOld-38,321
APING APPLICATION NUMBER: GOld-38,321
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APING APPLICATION NUMBER: GOld-38,321
APING APPLICATION NUMBER: GOld-38,321
APING APPLICATION NUMBER: GOld-38,396
APING APPLICATION NUMBER: GOld-38,396
APING APPLICATION NUMBER: GOld-38,396
APING APILE COOL-10-06
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2885 GAAGTGGACCTCTACAGAATGAACAGCCAGGACAAGCTGGGCTCACTGTGTGCTACCGG 2826
                                                                                                                                                                                                                                                                                                                                                                                                                              2705 CAGAAC-----CGTGAAGAGGCTGTGGGCTCTTCTAACCAGTGAAGAAATAAAAACTTT 2652
2945 CCAAATGACTACATTGGAGACATCCATCAGGAGATGGACAGGGAGGAGGAGCTGGAGCTGGAG 2886
                                                                                                                                                                                                                                                                    174 GluGlySerGly---LeuLysValGlyAspGlnIleLeuGluValAsnGlyArgSerPhe 192
                                                                                                                                                         154 GlyGlyAlaGluTyrGlyLeuGlyIleTyrIleThrGlyValAspProGlySerGluAla 173
                                                                                                                                                                                                                                                                                                                                                                             193 LeuAsnIleLeuHisAspGluAlaValArgLeuLeuLysSerSerArgHisLeuIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 ThrValLysAspValGlyArgLeuProHisAlaArgThrThrValAspGluThrLysTrp
                                                 140 LeuVal-----LeuGlyAspGlyArgSerLeuGlyLeuThrIle-----Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24, Application US/09964956
Publication No. US20040043926A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gerlach, Valerie L
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
APPLICANT: Stone, Isabelle
APPLICANT: Stone, Brik
APPLICANT: Guncher, Brik
APPLICANT: Ellerman, Karen
APPLICANT: Alsobrook II, John P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2606 ATGGATGATGACÁGG 2592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3245 CAAATTCATGACAGGATTATTGAGGTCAACGGCAGAGACTTATCCAGAGCAACTCATGAC 3186
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3065 CAAACCGACAICACCTITGAACAIAICAIGGCCCICACIAAGAIGICCICTCCCAGCCCA 3006
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                                                                                                                                              3365 CTGGGATTCAATATTATTGGTGGCCGACCGAGTGTAACCACGATGGATCATCCAGT 3306
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193 LeuAsnIleLeuHisAspGluAlaValArgLeuLeuLysSerSerArgHisLeuIleLeu 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 ArgValGlyAspGlnIleLeuArgValAsnAspLysSerLeuAlaArgValThrHisAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GluAlaValLysAlaLeuLysGlySerLysLys----LeuValLeuSerValTyr----- 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hyseq Inc
APPLICANT: Hyseq Inc
TILE OF INVENTION: NO. US20040053248Alel Nucleic Acids and Polypeptides
FILE REFERENCE: 784PCT
CURRENT APPLICATION NUMBER: US/10/296,115
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US09/488,725
PRIOR APPLICATION NUMBER: US09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 1478
SEQ ID NO 496
LENGTH: 4235
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                                                    2705 CAGAAC-----CGTGAAGAGGCTGTGGCTCTTCTAACCAGTGAAGAAATAAAACTTT
                                                                                                        213 ThrValLysAspValGlyArgLeuProHisAlaArgThrThrValAspGluThrLysTrp
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                    2606 ATGGATGATGACAGG 2592
                                                                                                                                                                                                                233 IleAlaSerSerArg 237
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46.42%
28.30%
15.31%
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Best Local Similarity:
Query Match:
DB:
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US-10-296-115-496/c
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-296-115-496
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APPLICANT: Shinkets, Richard A
TITLE OF INVENTION: NO. US20040043926Alel Proteins and Nucleic Acids Encoding Same
TITLE OF INVENTION: NO. US20040043926Alel Proteins and Nucleic Acids Encoding Same
TITLE OF INVENTION: NO. US20040043926Alel Proteins and Nucleic Acids Encoding Same
CURRENT APPLICATION NUMBER: US/09/964,956
PRIOR APPLICATION NUMBER: 60/235,631
PRIOR APPLICATION NUMBER: 60/235,633
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,064
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,065
PRIOR APPLICATION NUMBER: 60/236,066
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
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PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
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                                                                                                                1954
                                                                                                                                                                                                                                                                                              1835 TGCATTCGTGGACAGATTTTTGTCAAGACCATCTTCCCAAATGGATCAGCTGCA 1894
                                                                                                                                                              211
                                                                                                                                                                                                                                                  LeuThryalLysAspValGlyArgLeuProHisAlaArg-----ThrThrValAspGlu 229
                                                                     174 GluGlySerGlyLeuLysValGlyAspGlnIleLeuGluValAsnGlyArgSerPheLeu
                                                                                                              1895 GAGGACGGAAGACTTAAAGAAGGTGATGTGAATCCTAGATGTAAATGGAATACCAATAAAG
                                                                                                                                                            194 AsnileLeuHisAspGluAlaValArgLeuLeuLysSerSerArgHis-----LeuIle
                                                                                                                                                                                           230 ThrLysTrplleAlaSerSerArglleArgGluThrMetAlaAsnSerAlaGly---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2135 GATGAAĠĠĊAGTŤĊŤTCATCCTGGGTCGGAAGĀĊĊĊŤĠĠĠ 2176
                                                                                                                                                                                                                                                                                                                                                                                                                                    248 ---SerGlyHisSerAlaArgSerAsnLeuGlnThrProGly 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/237,434
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-05
PRIOR PILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/238,399
PRIOR APPLICATION NUMBER: 60/238,396
PRIOR APPLICATION NUMBER: 60/238,396
PRIOR FILING DATE: 2000-10-06
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FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/236,135
FILING DATE: 2000-09-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26, Application US/09964956 Publication No. US20040043926A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Padigaru, Muralidhara
Kekuda, Ramesh
Spytek, Kimberly A
Leach, Martin D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alsobrook II, John P
Lepley, Denise M
Burgess, Catherine E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gerlach, Valerie L
MacDougall, John R
Smithson, Glennda
Millet, Isabelle
Stone, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gunther, Erik
Ellerman, Karen
Grosse, William M
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              PRIOR APPLICATION NUMBER: 60/276,667
PRIOR FILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-05-31
PRIOR FILING DATE: 2001-05-31
PRIOR PILING DATE: 2001-05-31
PRIOR PELING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 127
SOOTWARE: PATENTIN Ver. 2.1
SEQ ID NO 24
LENGTH: 8640
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PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 60/304,868
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 127
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
LENGTH: 8640
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                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-956-26
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2075 ATGAGCAGATCCGCCTCCCCGAACTTCAATACCAGTGGGGGAGCCTCGGCGGAGGTTCC 2134
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174 GluGlySerGlyLeuLysValGlyAspGlnIleLeuGluValAsnGlyArgSerPheLeu 193
                                                    194 AsnileLeuHisAspGluAlaValArgLeuLySSerSerArgHis-----LeuIle
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## GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

April 22, 2004, 00:07:22; Search time 2513 Seconds (without alignments) 3089.601 Million cell updates/sec US-10-078-090-151 1326 1 LRRAKAHEGLGFSIRGGSEH......TWANSAGSGHSARSNLQTPG 260 27513289 segs, 14931090276 residues Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries 7.00 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext gorden general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general general Minimum DB seq length: 0 Maximum DB seq length: 200000000 em_esthum: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

HTC 19-NOV-2003	cDNA clone						Euteleostomi;	Homo.	
4569 bp mRNA linear HTC 19-NOV-2003	protein CIP98, mRNA retained intron.						Craniata; Vertebrata;	Catarrhini; Hominidae	
BC014524 4569 b	Homo sapiens CASK-interacting protein CIP98, mRNA (cDNA clone IMAGE:3834205), with apparent retained intron.	BC014524	BC014524.1 GI:17939549	HTC.	Homo sapiens (human)	Homo sapiens	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 4569)
RESULT 1 BC014524 LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE

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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetcow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carnindi, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McKean, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Halle, S., Garcia, A.M., Young, A.C., Shevohenko, Y.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevohenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E.,
Schnerch, A. Schein, J. E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse CDNA sequences
105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAL Plate: 14 Row: f Column: 19 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LeulrgArgAlaLysAlaHisGluGlyLeuGlyPheSerlleArgGlyGlySerGluHis 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 4569)
Strausberg,R.
Direct Submission
Submitted (24-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs.remant: DCTD/DTP
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Present Strate by: The I.W.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
Anup Madan@systemsbiology.org
Anup Madan, Jessica Fahay, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analysis clone has the following problem: retained intron.

Location/Qualifiers

1. 4569

| 1.4569
| / Adailyse="Homo sapiens" |
| / Adailyse="mRNA" |
| / Adailyse="mRNA" |
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| / Lib= NHH MGC_9" |
| / Liba host="0.000" |
| / Note="0.000" |
| / Note="0.000" |
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Matches:
Conservative:
Indels:
Gaps:
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1261.50
96.17%
95.79%
95.14%
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
JOURNAL
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MEDLINE
PUBMED
                 AUTHORS
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COMMENT
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602 bp mRNA linear EST 20-OCT-2000 60513147F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914675 5', mRNA sequence.
BE8990168
BE890168.1 GI:10348220
EST.
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                                                                                                                    1761
                                                                                                                                                                                                             100
                                                                                                                                                                                                                             1822 CGCATCCCTGGGGGCTACGTCACCACCATCTACACCTGGGTGGACCCGCAGGGCCGC 1881
                                                                                                                                                                                                                                                                                                                                                                                        141 ValLeuGlyAspGlyArgSerLeuGlyLeuThrlleArgGlyGlyAlaGluTyrGlyLeu 160
1582 TTGCGGCGTGCCAAGGCCCACGAGGCTTGGGCTTCAGCATCCGTGGGGGCTCGGAGCAC 1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BST.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
I (bases 1 to 602)
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                         09
                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                            201 ValargieuleulysSerSerArgHisLeulleLeuThrVallysAspValGlyArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 GlylleTyrIleThrGlyValAspProGlySerGluAlaGluGlySerGlyLeuLySval
                                                 81 ArgileProGlyGlyTyrValThrAsnHisIleTyrThrTrpValAspFroGlnGlyArg
                               21 GlyValGlyIleTyrValSerLeuValGluProGlySerLeuAlaGluLysGluGlyLeu
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Matazoa; Chordata; Sciurognathi; Muridae; Murinae; Muscryota; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Muscryota; Mateori, Coffee (1909)

Si NIH-Moch tip://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: The Cepko Laboratory

Contact: Robert Straved by: The I.M.A.G.E. Consortium (LINL)

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Inoyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Http://image.llhl.gov

Plate: LLAMIBIS ov m. column: 07
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/db xref="teaxon:10090"
/db xref="teaxon:10090"
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/note="Insert size 3.3 kb. Library enriched for Average insert size and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                  651 bp mRNA linear EST 20-SEP-2001
NIH_MGC_94 Mus musculus cDNA clone IMAGE:5361582 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 LeuGlnGlyGlyAspGluLysLysValAsnLeuValLeuGlyAspGlyArgSerLeuGly 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuThrileArgGlyGlyAlaGluTyrGlyLeuGlyIleTyrIleThrGlyValAspPro 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysLysLeuValLeuSerValTyrSerAlaGlyArgileProGlyGlyTyrValThrAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 GinproHisGlyGlyAlaLeuArgGlnGlnGluGlyAspArgArgSerThrLeuHisLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 651
Location/Qualifiers
                                                   603353931F1 NIH_MGC_94 PmRNA sequence.
BI732824
BI732824.1 GI:15709837
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                              LOCUS
DEFINITION
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AUTHORS
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COMMENT
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cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9736 row: m column: 12 Plate: LLAM9736 row: m column: 12 High quality sequence stop: 602.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E. I (Mases 1 to 729) Mus. S. II (Mases 1 to 729) Mus. S. II (Mases 1 to 729) Mus. S. II (Mases 1 to 729) Mus. S. II (Mases 1 to 729) Mus. S. II (Mases 1 to 729) Mus. S. II (Mases 1 to 729) Mus. S. II (Mases 1 to 729) Mus. S. II (Mases 1 to 729) Mus. S. II (Mases 1 to 729) Mus. S. II (Mases 1 to 729) Mus. Sequencing Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
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IMAGE:6816389 5', mRNA sequence.
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                                                        US-10-078-090-151 (1-260) x BX390092 (1-905)
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/clone="let strand cDNA was primed with a NoII-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with NoI I and cloned into the NoI I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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CTCACGATCCGAGGTGGAGCAGAGTACGGCCTTGGCATTTACATCACTGGTGGACCCA 361
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1. (bases 1 to 905)

1.i., M.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

Unpublished (2001)
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ACCESSION VERSION KEYWORDS

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FEATURES

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Homo sapiens (human)

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Lobaes 1 to 693)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CLONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop; 643.

High quality sequence stop; 643.
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                                                                                                  BF969269 101H_MGC_84 Homo sapiens cDNA clone IMAGE:4358158 5',
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/strain="C57BL/6"
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Email: poustka@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF

ONF to reduce studied state of the Same hybridiaation matrix with a partery of 200 8mer oligonucleotides are grouped into clusters. One clone per ONF cluster is salected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well as the coordinates of the other clones assigned to the same ONF cluster as the clone from which the above EST is generated is available at the sea urchin project web site at: http://www.molgen.mpg.de/ag seaurchin/. cDNA clones and filters are distributed via the Resource Center/Primary Database of the German Human Genome Project (http://www.rzpd.de)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265 AGGAGTACCCTCCACCTCCTGCAGAGTGGGAGAAAAAGGTGAACCTGGTGTTGGGG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 AspGlyArgSerLeuGlyLeuThrIleArgGlyGlyAlaGluTyrGlyLeuGlyIleTyr 163
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Poustka, A.G., Groth, D., Hennig, S., Thamm, S., Cameron, A., Beck, A., Groth, R., Herwig, R., Panopoulou, G. and Lehrach, H. Generation, amotation, evolutionary analysis, and database integration of 20,000 unique sea urchin EST clusters Genome Res. 13 (12), 2736-2746 (2003)
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PCRARAB: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP) 5'-seq
PORWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP) 3'-seq
Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' psport3/86
High quality sequence stcp: 643.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 AAGGCTCTCAAAGGCTCCAAGAAGCTGGTGTCTGTATACTCAGCTGGGGGGTATCCCA
                                                                                                                                                                                                                          GlyGlyTyrValThrAsnHislleTyrThrTrpValAspProGlnGlyArgSerIleSer
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Eukaryota, Metazoa, Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea, Eucechinoidea; Echinoidea; Echinoidea; Ethinoidea; Echinoidea; Echinoidea; Echinoidea; Echinoidea; Echinoidea; Echinoidea; Echinoidea; Ethinoidea;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 IleThrGlyValAspProGlySerGluAlaGluGlySerGlyLeuLysVal 180
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Max-Planck-Institut fuer Molekulare Genetik
Ihnestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
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/mol_type="mRNA"
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MACOGUE: 90243230 5', mRNA sequence.
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                                                                                                                                                                                                                          GlyAspArgArgSerThrLeuHisLeuLeuGlnGlyGlyAspGluLysLysValAsnLeu 140
                                                                                                                                                                                                                                                                                                                              395 GGTGACCGGAGGAGCACCCTGCACCTCCTGCAAGGAGGGATGAGAAAAAAGGTGAGTGGG 454
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                                                                                                          335 Adcarciccoaccercesecerececeaececases
SerIleSerProProSerGlyLeuProGlnProHisGlyGlyAlaLeuArgGlnGlnGlu
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              141 ValLeuGlyAspGlyArgSerLeu 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  455 Graggaaaggaagccagccrcrc 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CB209310.1 GI:28250873
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94.16%
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No.:

ORIGIN

Query Match

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                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                       Confact: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 7ZB
Tel: +44(0):51-795-431
Fax: +44(0):51-795-4431
Fax: +44(0):51-795-4431
Fax: +44(0):51-795-4431
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F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Wale & female"
/tissue_type="Muscle"
/dev stage="Adult"
/lab_host="s.coli | Blectromax DH10B"
/lab_host="s.coli | Blectromax DH10B"
/lab_host="coli | Blectromax DH10B"
/labe=lib="Carp muscle library 1"
/note="Vector: pTriplEx2; Site 1: Sfil GGCCATTACGGCC; Site 2: Sfil GGCGCCTCGGCC; Serially subtracted cDNA library prepared from muscle of warm, cold and hypoxia challenged animals"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pGlyArgSerLeuGlyLeuThrileArgGlyGlyAlaGluTyrGlyLeuGlyIeTyrIl
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                                                                                                                                                                                                                                                                                                                                                                                                 Crown
                             Cyprinus carpio (common carp)

Syprinus carpio

Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Eutellaction Cyprinis Carpio; Teleostei; Ostariophysi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cyprinicaes Cyprinidae; Cyprinus.

(bases 1 to 1160)

Gracey,A.Y., Fraser,E., Li,W. and Cossins,A.R.

Microarray and EST analysis of the carp (Cyprinus carpio)

Historicum and Long environmental stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysLysLeuValLeuSerValTyrSerAlaGlyArg-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .1160
| Organism="Cyprinus carpio"
|mol_type="mRNA"
|db_xref="taxon:7962"
|clone="34k21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [ndels:
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581.00
71.86%
60.30%
43.82%
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Best Local Similarity:
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DB:
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SOURCE
ORGANISM
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90
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AUTHORS
TITLE
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COMMENT
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/db_xref="taxon:7668"
/clone="WhYGp691D1336,MPI_SURUDI_38D13"
/tissue_type="whole larva"-
/dev_stage="larva 2-3 weeks"
/dev_stage="larva 2-3 weeks"
/deb_host="E.coli, XII blue"
/clone_lib="Sea_urchin larva cDNA_library MPMGp691"
/note="Vector: pSportl; Site_1: NotI; Site_2: SalI; Random primed and directlonally cloned in pSportl vector using a NotI (5'-pGACTATTCTAGATGCTGAGGGGGGGGGCGCCC (T)15-3' and a SalI s'- TCGACCCACGGGTCGG-3'adapters (Gibco BRL)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRATGCTAAATGATACACAGAATAGAAAGAGTGGTCTCAACCTCCTCAAGAACGGCGATG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        371 AAAAGAAGGTCAATGTTGTAGTGAATGAAGGAGAGAGTCTTGGTTTGATGATTCGAGGAG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lyAlaGluTyrGlyLeuGlyIleTyrIleThrGlyValAspProGlySerGluAlaGluG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 leLeuHisAspGluAlaValArgLeuLysSerSerArgHisLeuIleLeuThrVall 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 laLeuArgGlnGlnGluGlyAspArgArgSerThrLeuHisLeuLeuGlnGlyGlyAspG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          luLysLysValAsnLeuValLeuGlyAspGlyArgSerLeuGlyLeuThrileArgGlyG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 lySerGlyLeuLysValGlyAspGlnIleLeuGluValAsnGlyArgSerPheLeuAsnI 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||:::||| ||||||| CAGATRARARGAGAGACCAGATTATGCAGGTCAATGACATTCCATTTG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alAspProGlnGlyArgSerIleSerProProSerGlyLeuProGlnProHisGlyGlyA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 TGAACCCCAAGGGGGGAGTGTGTCCCCTCCACGGACGTC---GACCCCTTGGTGGGA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTGGGGCGGAGCATTCGGTGGGGAATCTTTGTGTCGCTGGTGGAACCAAACAGTTATGGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 laArgValThrHisAlaGluAlaValLysAlaLeuLysGlySerLysLysLeuValLeuS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 ervalTyrSerAlaGlyArglleProGlyGlyTyrValThrAsnHislleTyrThrTrpy 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyGlySerGluHisGlyValGlyIleTyrValSerLeuValGluProGlySerLeu--A 35
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CF661317.1 GI:37558475
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EST.

Danio rerio (zebrafish)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Atinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidas; Danio.

El (Bases I to 870)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

At Onpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rmu0A07 Bethesda, MD 2092

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Leonard I. Zon, M.D.

CDNA Library Preparation: Invitrogen Corp

CDNA Library Preparation: Invitrogen Corp

CDNA Library Preparation: Invitrogen Corp

CDNA Library Preparation: Invitrogen Corp

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

High quality sequence stop: 567.

High quality sequence stop: 567.
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                       115 AlaLeuArgGlnGlnGluGlyAspArgArgSerThrLeuHisLeuLeuGlnGlyGlyAsp 134
                                                            185 ACCCTGAGACAGCATGAAGATGATCGAGGAGTGCCCTACACCTCCTGCAGAGTGGAGT
                                                                                                                                                                                                                                                                                                          251 ------AAGGTTGGGGACCAGATTCTGGAGGTGAACGGGCGGAGCTTTCTCAGC
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AGENCOURT 14627806 NCI CGAP ZKidl Danio rerio cDNA clone IMAGE:6961736 5', mRNA sequence.
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CD760225.1 GI:32344518
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                                                                 uLysSerSerArgHisLeuIleLeuThrValLysAspValGlyArgLeuProHisAlaAr 224
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CACCGGAGTGGACCGAGGGTCTGCTGCAGAGTACAGCGGACTAAAGGTAGGGGGATCAGAT 665
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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/mol type="mRNA"
/mol type="mRNA"
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/clone libe-trpg2 (10294)"
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peneal gland brain region"
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Plate: 00003 row: g column: 7. Location/Qualifiers
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Rattus norvegicus
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Contact: Dan Fitzpatrick
Amgen, Inc
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Rattus norvegicus (Norway rat)
Rattus norvegicus
Rattus norvegicus
Rattus norvegicus
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Amgen EST Program.

Amgen Rat EST Program.

Amgen (2003)

Contact: Dan Fitzpatrick

Amgen, Inc
One Hitzpatrick

Amgen, Inc
One 447-4881

Fel: 805 447-4881

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AMCNNUC:SRPG2-00029-A8-A srpg2 (10238) Rattus norvegicus cDNA clone srpg2-00029-a8 5', mRNA sequence.
CB693399

CB693399

I 3:29750546

EST.
Rattus norvegicus (Norway rat.)
Rattus norvegicus (Norway rat.)
Rattus norvegicus Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Rodentia; Sclurognathi; Muridae; Murinae;
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peneal gland brain region"
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Amgen Rat EST Program
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Droublished (2001)

Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Contactory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-2 Suchino-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Email: genome-res@goc.riken.go.jp,
URL:http://genome-goc.riken.go.jp,
UR
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/clone_lib="RIKEN full-length enriched, 1 month neonate
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         RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
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/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="G630034G23"
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                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
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/tissue_type="peneal gland brain"
/clone_Iib="srpg2 (10238)"
/clone_Iib="srpg2 (10238)"
/clone_Iib="srpg2 (10238)"
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Matsuyama, T., Tto, M., Kawai, T., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okazaki, Y., Salto, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Tanaka, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y.
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Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00029 row: a column: 8.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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1 (bases 1 to 325)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., Simpson,D.H., Glyman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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Pax: +55-11-2707001

Email: asimpsonaludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-NN1182-12100-011-1908&t2=2000-11-12&t4=1)
Seq primer: puc 18 forward
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RC3-NN1182-121100-011-g08 NN1182 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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